



QY 241 SLSLSTGYHKQEKSRLOGVLVNEILNKMKLATDPQKYKKLWMSANDTVSGIQMALD 300  
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Db 241 SLSLSTGYHKQEKSRLOGVLVNEILNKMKLATDPQKARKLWMSADTVSGIQMALE 300  
301 VVNGVLVPASCHMHELVDKGFVEMVYRRENOEPYPLTLPCCTSCPLERFAELLD 360  
:::|||||  
Db 301 LVNGLLPPYASCHIELVELVDNGTGVEMVYRRENETONEPPLTLPLCTSCPLERFAELLD 360  
361 PVIPODMATECMATSSHOGTV 381  
|||||  
Db 361 PVIPODMATECMGTSNHQASL 381  
RESULT 2  
JH0610  
acid phosphatase (EC 3.1.3.2) ACP precursor [validated] - human  
N:Alternate names: acid phosphatase, prostator, orthophosphoric monoester phosphohydrolase  
C:Species: Homo sapiens (man)  
C:Date: 17-Aug-1992 #sequence-revision 01-Dec-1995 #text-change 08-Dec-2000  
C:Accession: JH0610; J50693; A38608; S01331; A32419; S11147; S38863; S41251; S17042; S42  
R:Shier, F.S.; Li, S.S.L.  
Biochem. Biophys. Res. Commun. 184, 1468-1476, 1992  
A:Title: Structure of human prostatic acid phosphatase gene.  
A:Reference number: JH0610; MUID:92272747  
A:Accession: JH0610  
A:Molecule type: DNA  
A:Residues: 1-386 <SHN>  
A:Cross-references: GB:M97580; GB:M97581; GB:M97582; GB:M97583; GB:M97584; GB:M97585; GB:M97586; GB:M97587; GB:M97588; GB:M97589; GB:M97590; GB:M97591; GB:M97592; GB:M97593; GB:M97594; GB:M97595; GB:M97596; GB:M97597; GB:M97598; GB:M97599; GB:M97600; GB:M97601; GB:M97602; GB:M97603; GB:M97604; GB:M97605; GB:M97606; GB:M97607; GB:M97608; GB:M97609; GB:M97610; GB:M97611; GB:M97612; GB:M97613; GB:M97614; GB:M97615; GB:M97616; GB:M97617; GB:M97618; GB:M97619; GB:M97620; GB:M97621; GB:M97622; GB:M97623; GB:M97624; GB:M97625; GB:M97626; GB:M97627; GB:M97628; GB:M97629; GB:M97630; GB:M97631; GB:M97632; GB:M97633; GB:M97634; GB:M97635; GB:M97636; GB:M97637; GB:M97638; GB:M97639; GB:M97640; GB:M97641; GB:M97642; GB:M97643; GB:M97644; GB:M97645; GB:M97646; GB:M97647; GB:M97648; GB:M97649; GB:M97650; GB:M97651; GB:M97652; GB:M97653; GB:M97654; GB:M97655; GB:M97656; GB:M97657; GB:M97658; GB:M97659; GB:M97660; GB:M97661; GB:M97662; GB:M97663; GB:M97664; GB:M97665; GB:M97666; GB:M97667; GB:M97668; GB:M97669; GB:M97670; GB:M97671; GB:M97672; GB:M97673; GB:M97674; GB:M97675; GB:M97676; GB:M97677; GB:M97678; GB:M97679; GB:M97680; GB:M97681; GB:M97682; GB:M97683; GB:M97684; GB:M97685; GB:M97686; GB:M97687; GB:M97688; GB:M97689; GB:M97690; GB:M97691; GB:M97692; GB:M97693; GB:M97694; GB:M97695; GB:M97696; GB:M97697; GB:M97698; GB:M97699; GB:M97700; GB:M97701; GB:M97702; GB:M97703; GB:M97704; GB:M97705; GB:M97706; GB:M97707; GB:M97708; GB:M97709; GB:M97710; GB:M97711; GB:M97712; GB:M97713; GB:M97714; GB:M97715; GB:M97716; GB:M97717; GB:M97718; GB:M97719; GB:M97720; GB:M97721; GB:M97722; GB:M97723; GB:M97724; GB:M97725; GB:M97726; GB:M97727; GB:M97728; GB:M97729; GB:M97730; GB:M97731; GB:M97732; GB:M97733; GB:M97734; GB:M97735; GB:M97736; GB:M97737; GB:M97738; GB:M97739; GB:M97740; GB:M97741; GB:M97742; GB:M97743; GB:M97744; GB:M97745; GB:M97746; GB:M97747; GB:M97748; GB:M97749; GB:M97750; GB:M97751; GB:M97752; GB:M97753; GB:M97754; GB:M97755; GB:M97756; GB:M97757; GB:M97758; GB:M97759; GB:M97760; GB:M97761; GB:M97762; GB:M97763; GB:M97764; GB:M97765; GB:M97766; GB:M97767; GB:M97768; GB:M97769; GB:M97770; GB:M97771; GB:M97772; GB:M97773; GB:M97774; GB:M97775; GB:M97776; GB:M97777; GB:M97778; GB:M97779; GB:M97780; GB:M97781; GB:M97782; GB:M97783; GB:M97784; GB:M97785; GB:M97786; GB:M97787; GB:M97788; GB:M97789; GB:M97790; GB:M97791; GB:M97792; GB:M97793; GB:M97794; GB:M97795; GB:M97796; GB:M97797; GB:M97798; GB:M97799; GB:M97800; GB:M97801; GB:M97802; GB:M97803; GB:M97804; GB:M97805; GB:M97806; GB:M97807; GB:M97808; GB:M97809; GB:M97810; GB:M97811; GB:M97812; GB:M97813; GB:M97814; GB:M97815; GB:M97816; GB:M97817; GB:M97818; GB:M97819; GB:M97820; GB:M97821; GB:M97822; GB:M97823; GB:M97824; GB:M97825; GB:M97826; GB:M97827; GB:M97828; GB:M97829; GB:M97830; GB:M97831; GB:M97832; GB:M97833; GB:M97834; GB:M97835; GB:M97836; GB:M97837; GB:M97838; GB:M97839; GB:M97840; GB:M97841; GB:M97842; GB:M97843; GB:M97844; GB:M97845; GB:M97846; GB:M97847; GB:M97848; GB:M97849; GB:M97850; GB:M97851; GB:M97852; GB:M97853; GB:M97854; GB:M97855; GB:M97856; GB:M97857; GB:M97858; GB:M97859; GB:M97860; GB:M97861; GB:M97862; GB:M97863; GB:M97864; GB:M97865; GB:M97866; GB:M97867; GB:M97868; GB:M97869; GB:M97870; GB:M97871; GB:M97872; GB:M97873; GB:M97874; GB:M97875; GB:M97876; GB:M97877; GB:M97878; GB:M97879; GB:M97880; GB:M97881; GB:M97882; GB:M97883; GB:M97884; GB:M97885; GB:M97886; GB:M97887; GB:M97888; GB:M97889; GB:M97890; GB:M97891; GB:M97892; GB:M97893; GB:M97894; GB:M97895; GB:M97896; GB:M97897; GB:M97898; GB:M97899; GB:M97900; GB:M97901; GB:M97902; GB:M97903; GB:M97904; GB:M97905; GB:M97906; GB:M97907; GB:M97908; GB:M97909; GB:M97910; GB:M97911; GB:M97912; GB:M97913; GB:M97914; GB:M97915; GB:M97916; GB:M97917; GB:M97918; GB:M97919; GB:M97920; GB:M97921; GB:M97922; GB:M97923; GB:M97924; GB:M97925; GB:M97926; GB:M97927; GB:M97928; GB:M97929; GB:M97930; GB:M97931; GB:M97932; GB:M97933; GB:M97934; GB:M97935; GB:M97936; GB:M97937; GB:M97938; GB:M97939; GB:M97940; GB:M97941; GB:M97942; GB:M97943; GB:M97944; GB:M97945; GB:M97946; GB:M97947; GB:M97948; GB:M97949; GB:M97950; GB:M97951; GB:M97952; GB:M97953; GB:M97954; GB:M97955; GB:M97956; GB:M97957; GB:M97958; GB:M97959; GB:M97960; GB:M97961; GB:M97962; GB:M97963; GB:M97964; GB:M97965; GB:M97966; GB:M97967; GB:M97968; GB:M97969; GB:M97970; GB:M97971; GB:M97972; GB:M97973; GB:M97974; GB:M97975; GB:M97976; GB:M97977; GB:M97978; GB:M97979; GB:M97980; GB:M97981; GB:M97982; GB:M97983; GB:M97984; GB:M97985; GB:M97986; GB:M97987; GB:M97988; GB:M97989; GB:M97990; GB:M97991; GB:M97992; GB:M97993; GB:M97994; GB:M97995; GB:M97996; GB:M97997; GB:M97998; GB:M97999; GB:M98000; GB:M98001; GB:M98002; GB:M98003; GB:M98004; GB:M98005; GB:M98006; GB:M98007; GB:M98008; GB:M98009; GB:M98010; GB:M98011; GB:M98012; GB:M98013; GB:M98014; GB:M98015; GB:M98016; GB:M98017; GB:M98018; GB:M98019; GB:M98020; GB:M98021; GB:M98

A.Molecule type: DNA  
A.Residues: 1-40 <BR>  
A.Cross-references: EMBL:X71391; NID:g416530; PIDN:CAA50514.1; PID:g416531  
R.Vitkkunen, P.H.; Hebejy, P.; Palvinio, J.T.; Birt, E.; Forvarl, K.; Taavitsainen, P.  
Submitted to the EMBL Data Library, September 1993  
A.Description: Structural organization of human and rat prostate-specific acid phosphatase in the human gene promoter.  
A.Reference number: s41251  
A.Molecule type: DNA  
A.Accession: S41251  
A.Residues: 1-40 <VR>  
A.Cross-references: EMBL:X74961; NID:g439657; PIDN:CAA52913.1; PID:g439658  
R.Lee, H.; Chu, T.M.; Li, S.S.L.; Lee, C.  
Biochem. J. 277, 759-765, 1991  
A.Title: Homodimer and heterodimer subunits of human prostatic acid phosphatase.  
A.Reference number: SI7042; MUID:91336999  
A.Accession: SI7042  
A.Status: preliminary  
A.Molecule type: protein  
A.Residues: 33-49 <LE>  
R.Banas, B.; Blaschke, D.; Filler, F.; Hoerz, W.  
Blochim. Biophys. Acta 1217, 188-194, 1994  
A>Title: Analysis of the promoter of the human prostatic acid phosphatase gene.  
A.Reference number: S42730; MUID:94153995  
A.Accession: S42730  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-40 <BA>  
A.Cross-references: GB:X71391; NID:g416530; PIDN:CAA50514.1; PID:g416531  
R.Sharief, F.S.; Li, S.S.  
Biochem. Mol. Biol. Int. 33, 561-565, 1994  
A>Title: Nucleotide sequence of human prostatic acid phosphatase ACP gene.  
A.Reference number: I37175; MUID:95038536  
A.Accession: I37175  
A.Status: preliminary; translated from GB/EMBL/DDBU  
A.Molecule type: DNA  
A.Residues: 1-386 <RE>  
A.Cross-references: EMBL:U07097; NID:g515995; PIDN:AAB60640.1; PID:g515997  
C.Comment: This protein is synthesized under androgen regulation by epithelial cells  
C.Genetics:  
A.Gene: GDB:ACPP  
A.Cross-references: GDB:119644; OMIM:171790  
A.Map position: 3q21.3-3q25.2  
A.Introns: 40/3; 72/3; 101/3; 152/3; 185/3; 216/3; 260/3; 288/3; 323/2  
C.Function:  
A.Description: catalyzes the hydrolysis of a wide range of phosphate esters  
C.Superfamily: mammalian acid phosphatase  
C.Keywords: glycoprotein; phosphonitidine; phosphoprotein; phosphoric monoester hydrolase  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:33-386/Product: acid phosphatase ACP #status experimental <MAT>  
F:43/86/Active site: Arg #status predicted  
F:44/Active site: His (phosphonitidine intermediate) #status predicted  
F:94/220/333/Binding site: carbohydrate (asn) (covalent) #status experimental  
F:161-372, 215-313, 347-351/Disulfide bonds: #status experimental

Query Match 80.7%; Score 1661.5; DB 1; Length 386;  
Best Local Similarity 81.6%; Pred. No. 2.3e-126;  
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

DY 1 MGAVPLPSPTSTSLGFLLLSLCLDPC-QAKELKFTLVFRHGDRCPIETFPDPITE 59  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 1 MRAAPLLLAARASLSLGFLFLFFWLDRSYLAKELEKTIVLPFRHDSRPIDTFPDPIKE 60  
  
DY 60 SSWPGFGQLTQWGMEOHYELGSYTRKRYGRFLNDJYNHOIYIRSTVDRTLSAMTNL 119  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 61 SSWPGFGQLTQWGMEOHYELGSYTRKRYGRFLNDJYNHOIYIRSTVDRTLSAMTNL 120  
  
DY 120 ALAFPEEGISTNNPRLNQPITPVHTVLSSEDRLLTLPRDPCRRELKSETLSEEPFKR 179  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 121 ALAFPEEGISTNNPRLNQPITPVHTVLSSEDRLLTLPRDPCRRELKSETLSEEPFKR 180  
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DY 180 LHPYSKFDLTSSLEGPDODLFCIGMSKYVPDLFCESYHNFTLCSWMATEDMIRKTELSE 239

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||||| : || ||| |||||||||||||:||||||||||||| ||| |||
Db 181 LHPKDFIATIGKISGLHGDLFGIMSKYVDPLDCEVHNHTLPSPATNEDMTMLRELSE 240
OY 240 LSLSLVGIHKOKKSRLOGGVNLVETILKNKLATOPQKYKKLVMSAHDVTYSGLOMAL 299
Db 241 LSLSLVGIHKOKKSRLOGGVNLVETILKNKLATOPQKYKKLVMSAHDVTYSGLOMAL 300
OY 300 DVNNGVLPYASCHMMLYHDKGHFVEMYYRNFTONEPPTLPGLGTHSCPLEKFAELL 359
Db 301 DVNNGVLPYASCHMMLYHDKGHFVEMYYRNFTONEPPTLPGLGTHSCPLEKFAELL 360
OY 360 DVPVPODMATECMATSSHOQT 380
Db 361 GPVVPDMSTECMTNTHOGT 381

RESULT 3
acid phosphatase (EC 3.1.3.2) ACP2 precursor [validated] - human
N:Alternate names: acid phosphatase, lysosomal
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 01-Dec-1995 #text_change 08-Dec-2000
C:Accession: S06167; S05525; S01155
R: von Figura, K.
Submitted to the EMBL Data Library, June 1989
A:Reference number: S06167
A:Accession: S06167
A:Molecule type: DNA
A:Residues: 1-423 <YON>
A:Cross-references: EMBL:X15525; NID:934239; PIDN:CAA3542.1; PID:91199524
R: Geier, C.; von Figura, K.; Pohlmann, R.
Eur. J. Biochem. 183, 611-616, 1989
A:Title: Structure of the human lysosomal acid phosphatase gene.
A:Reference number: S05525; MUID:89377828
A:Accession: S05525
A:Molecule type: DNA
A:Residues: 1-29 <GET>
R: Pohlmann, R.; Krentler, C.; Schmidt, B.; Schroeder, W.; Lorkowski, G.; Culley, J.; Merz
EMBO J. 7, 2333-2350, 1988
A:Title: Human lysosomal acid phosphatase: cloning, expression and chromosomal assignment
A:Reference number: S01155; MUID:89052645
A:Accession: S01155
A:Molecule type: mRNA
A:Residues: 1-423 <POH>
A:Cross-references: EMBL:X12548; NID:934262; PIDN:CAA31064.1; PID:934263
A:Note: Part of this sequence, including the amino end of the mature protein, was confir
C:Genetics:
A:Gene: GDB:ACP2
A:Cross-references: GDB:118963; OMIM:171650
A:Map position: 11p11.2-11p11.11
A:Insertions: 38/3; 70/3; 99/3; 150/3; 183/3; 213/3; 258/1; 285/3; 321/2; 380/1
C:Function:
A:Description: catalyzes the hydrolysis of a wide range of phosphate esters
C:Superfamily: mammalian acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydroly
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-423/Product: acid phosphatase ACP2 #status experimental <MAP>
F:4/Active site: Arg #status predicted
F:42/Active site: His (phosphohistidine intermediate) #status predicted
F:92,133,167,177,191,267,322,331/Binding site: carboxydrate (Asn) (covalent) #status pre
F:159-370,212-310,345-349/Dissulfide bonds: #status predicted

Query Match 49.6%; Score 1022.5; DB 1; Length 423;
Best Local Similarity 51.4%; Pred. No. 9.2e-75;
Matches 189; Conservative 62; Mismatches 112; Indels 5; Gaps 3;
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Db 73 MLOHMELOALRQRYHGFPLNTSYHROEVYRSJFDRTLMSAEANLAGLFPNNGMORNP 132
OY 134 RLMOPIPVHTVSLSEDRLLYLPFRDCPRFEELKSETLSEEFKLRLHPYKSLDITLSSL 193
Db 133 NISQPIPVHTVPTTEDRLKLFPLGCPRYEQLOLNETRQRPYONESSRNAQFIDMVA NE 192
OY 194 SCFDDDLFGIMSKYVDPLDCEVHNHTLPSPATNEDMTMLRELSESLSLVGIHKOKE 253
Db 193 TGLTDLTLETVMN--VYDTLFCEDQTHGLRLPPWASPOQTMRSLRKDPSFRFLFGIYQDAE 251
OY 254 KSRLGGVNLVETILKNKLATOPQKYKKLVMSAHDVTYSGLOMALDVYNGVLPYASCH 313
Db 252 KARLGGVNLVETILKNKLATOPQKYKKLVMSAHDVTYSGLOMALDVYNGVLPYASCH 311
OY 314 MMEYLHDKGHF--VEMYYRNFTONEPPTLPGLGTHSCPLEKFAELLDPVVPDMATECM 372
Db 312 IFELLYQEDSGNFSEVEMYYRNFTONEPPTLPGLGTHSCPLEKFAELLDPVVPDMATECM 371
OY 373 ATSSHOQT 380
Db 372 LASGPADT 379

RESULT 4
acid phosphatase (EC 3.1.3.2) precursor - mouse (fragment)
S14742
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Mar-2000
C:Accession: S14742
R: Geier, C.; von Figura, K.; Pohlmann, R.
Biochem. Biophys. Res. Commun. 199, 301-304, 1991
A:Title: Molecular cloning of the mouse lysosomal acid phosphatase.
A:Reference number: S14742; MUID:91282986
A:Accession: S14742
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-421 <GET>
A:Cross-references: EMBL:X57199; NID:952870; PIDN:CAA0485.1; PID:952871
C:Superfamily: mammalian acid phosphatase
C:Keywords: lysosome; phosphoric monoester hydrolase

Query Match 49.5%; Score 1020.5; DB 2; Length 421;
Best Local Similarity 51.4%; Pred. No. 1.3e-74;
Matches 187; Conservative 66; Mismatches 106; Indels 5; Gaps 3;
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RESULT 5  
A33395 acid phosphatase (EC 3.1.3.2) precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 22-Jun-1999  
C:Accession: A33395  
R:Himeno, M.; Fujita, H.; Noguchi, Y.; Kono, A.; Kato, K.  
Biochem. Biophys. Res. Commun. 162, 1044-1053, 1989  
A:Title: Isolation and sequencing of a cDNA clone encoding acid phosphatase in rat liver  
A:Reference number: A33395; MUID:89350910  
A:Accession: A33395  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-423 <H1D>  
A:Cross-references: GB:M27893; NID:g202933; PIND:AAAA0474.1; PID:g202934  
C:Superfamily: mammalian acid phosphatase  
C:Keywords: phosphohistidine, phosphoprotein, phosphoric monoester hydrolase  
F:41/Active site: Arg #status predicted  
F:42/Active site: His (phosphohistidine intermediate) #status predicted

Query Match	49.5%;	Score 1019.5;	DB 2;	length 423;
Best Local Similarity	51.9%;	Pred. No. 1.6e-74;		
Matches 189;	Conservative 61;	Mismatches 109;	Indels 5;	Gaps 3;

[illegible]

RESULT 6  
S64682  
acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 17-Mar-2000  
C:Accession: S64682; S64681  
R:Chung, H.J.; Shafer, C.; MacIntyre, R.  
Mol. Gen. Genet. 250, 635-646, 1996  
A:Title: Molecular characterization of the lysosomal acid phosphatase from *Drosophila melanogaster*  
A:Reference number: S64681; MUID:96194627  
A:Accession: S64682  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-438 <CHU>  
A:Accession: S64681  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA

A:Residues: 1-31, 'Y', 33-438 <CHW>  
A:Genetics:  
A:Gene: FlyBase:AcpH-1  
A:Cross-references: FlyBase:FBgn0000032  
C:Superfamily: mammalian acid phosphatase  
C:Keywords: phosphoric monoester hydrolase  
F:31-433/Domains: signal sequence #status predicted <SIG>  
F:31-433/Product: acid phosphatase AcpH-1 #status predicted <MAT>

Query Match	30.0%;	Score 617;	DB 2;	Length 438;
Best Local Similarity	38.1%;	Pred. No. 5e-42;		
Matches 141;	Conservative 59;	Mismatches 114;	Indels 56;	Gaps 14;

Oy	28	PQAKELKFLVLRNHRDGRGTEFFRPDPITRESS--WQGVBQLTQMOMEONHLELGASTIRK	86
Dd	45	PGQ---LKFVVHYIYRKHGGRTVEVDPRIDPWDRKEFWETGMDDLITNGKOEHYUJGKMLRN	100
Oy	87	RYGRLNTYKHDOUYISTDVDRTRLSAMNLLAALRRPREGISITWNRLMOPRLPVTVS	146
Dd	102	KYSNLPLPTYSNENITYOSTVDYDTILMSAGSNLAGLYEPQSGEDIMWTDINMOPRIHTSP	161
Oy	147	LSEDLRLLPFRDCPRFE-ELKSETLSESEELRL-----HPYKSFLT	189
Dd	162	EREDPIIAAK-APCAVYUELAS--LESSPEFKALTKEHNRLFAYLSEKGGRPYKTIDA	218
Oy	190	LSLSLGFDDQLFGIWSKVYVRPLFCESYNHNTPLSMATEDAMIKLSELSTLS--LYG	247
Dd	219	-----OYLNTLTLEIENYNTLTWKTK-----KYVGREBLTYVSNAFA	257
Oy	248	IHKOKK-SRLGGVLVEILLNKML-----ATOPKKKLVMASAHOTVSGLOMALDYV	302
Dd	258	ISSYTRKLARLACAGBLADITFORREKSSGSLKD--RSKMVSAHOTVVAASVLANAKLF	315
Oy	303	NGVLRYVASCHMMELYHDK-GGHFVEMYEMRNETOBERPLTLPCGTHSCPLEKAEBLLD	361
Dd	316	ELHSPPYACIMBELRVDETWTPLVSIFYKNYTA-EPLRLPIDECGFSCLPTKLMNIYED	374
Oy	362	VIPODMATEC	371
Dd	375	VLPIVDMEREK	384

RESULT 7  
T32457  
hypothetical protein T13B5.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text-change 17-Mar-2000  
C:Accession: T32457  
R:Maggi, L.  
submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid T13B5.  
A:Reference number: Z21172  
A:Accession: T32457  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-440 <MAG>  
A:Cross-references: EMBL:AF026211; PIDN:AMB71294.1; GSPDB:GN00020; CESP:T13B5.3.  
A:Experimental source: strain Bristol N2; clone T13B5  
C:Genetics:  
A:Gene: CESP:T13B5.3  
A:Map position: 2  
A:Introns: 25/3; 90/3; 125/3; 162/2; 242/3; 289/1; 328/3; 373/3; 404/3  
C:Superfamily: mammalian acid phosphatase

Query Match	23.6%	Score 487;	DB 2;	Length 440;
Best Local Similarity	33.8%	Pred. 1.5e-31;		
Matches 130;	Conservative 61;	No. Matches 144;	Indels 50;	Gaps 14;
QY	33 ELKFLVTFVHRHDDRIETFFPPDPTITSESSPQFCGLQTMWQMEQHYELGYSYTRKRY----	88		
DP	52 ELLLSOVVWRHGDRAPTGYPTDDPKHKEEMVPMGWSGLDGLGRVOOYALGRLIIKKYKVNST	111		





Db 519 VTDOPEKFNRTTDMKKORRMENDMTMOOLPWINEEDYINFAOQTYAPFKKFTCEGNGNPK 578  
QY 225 WATEDAMIKETSELSELSTLYGCIHKOKERSRLGGGLVINEILKNK-----IA 273  
Db 579 PSYD-----GIDIPQEVSTLGGCPFLWEIERGEREKTRCYADENCS 621  
QY 274 TQOPKYKLVMSAHDPTVSGLOMALDPUYNGV-----LPPYASCHMHELHYDKGH-FYE 327  
Db 622 IDYLKPLKFAYSSHDDLVALLVTLGITDVYKTVDGWPTSSSLITYEYISNGGNOSSVAK 681  
QY 328 MYENETONEBEYPLT--LPCGTHS--CPLEKEFAELDLVPJR--ODMAITECMATSSHOQTV 381  
Db 682 FLVYDNSNDNSNDVYTSQIPYCNGAQOYCAMSDFOINAYQFPLDYMILCTLSLSSISV 740

RESULT 13  
T16883  
hypothetical protein T16D1.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: T16883  
R:Bentley, D.  
submitted to the EMBL Data Library, October 1995  
A:Description: The sequence of C. elegans cosmid T16D1.  
A:Reference number: Z18597  
A:Accession: T16883  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-380 <BEN>  
A:Cross-references: EMBL:U39471; NID:g1041874; PID:g1041876; PIDN:AAA80132.1; CESP:T16D1  
A:Experimental source: strain Bristol N2  
C:Genetics:  
A:Gene: CESP:T16D1.2  
A:Introns: 34/3; 69/3; 137/3; 174/3; 278/1; 333/3  
A:Superfamily: mammalian acid phosphatase

Query Match	14.08;	Score 287.5;	DB 2;	Length 380;
Best Local Similarity	29.28;	Pred. No. 1.5e-15;		
Matches 98;	Conservative 47;	Mismatches 108;	Indels 83;	Gaps 15;

```

0Y      33 ELKFTVTVFRIGDGGPIETEPIDITSSN---POGSGOLWGMEDHVSLSYIKRY- 88
Db      28 KLMVAQIMRGGDTPIETHNDQPTENYMFGGGGWGLTIGRMQHMLQGKKLRARY 87,
0Y      89 -----GRELNDYKKHDQIYIRSTVDRIEMASMTL-----AAL----- 122
Db      88 NGOPYKFLNTTRYNOQLFIVSTGDKNRTLLAFSNMVCMEIRRRKHHPDLASLKCHYVG 147
0Y      123 --FP-----PEGISIWNPRLLOMPIPVHTSVLSSEDRLL-----YLPRDCRFEEKLSETL 171
Db      148 VDYPDVGVMPYG-----FWPILPHLTIPDAEDHLTLSDVNCPLDD-IHWMLAKTTDI 197
0Y      172 ESEFELKRLEHPKYSEFLDTLSSLGSSEFDQDLFGIWSKVAYDPFLCESVH-----NFLPSW 225
Db      198 VSANFY--NSSAVTSIIMGNLTNYCG-EEINPDNLMI-LYNALKITEKQYPAQFOKFT--PW 251
0Y      226 ATEDAMTKIKELSE-----LSLLSLGYIHKKQEKSRLOGGVLYNEILNNMKLATQ 275
Db      252 YTDSELFEQIDLVNSQVODFONGGLEEGKMVNGIDIGKITRKIRGGTLVNDIYHNMRKTQ 311
0Y      276 PQRYK-----KLVMSAHDTVTSGIQMALDV 301
Db      312 CSSNMGECECTYTNRLEKFAYSADHDTTLTYALFSLGV 347

```

RESULT 14  
T18945  
hypothetical protein C05C10.4 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T18945

R:Matthews, P.  
submitted to the EMBL data Library, February 1995  
A:Reference number: Z19049  
A:Accession: T18945  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-413 <WIL>  
A:Cross-references: EMBL:Z48178; PIDN:CAA88205.1; GSPDB:GN00020; CESP:C05C10.4  
A:Experimental source: clone C05C10  
C:Genetics:  
A:Gene: CESP:C05C10.4  
A:Map position: 2  
A:introns: 31/3; 96/3; 128/1; 155/3; 185/3; 255/1; 313/3; 360/3; 407/3  
C:Superfamily: mammalian acid phosphatase

Query Match	13.3%	Score 274;	DB 2;	Length 413;
Best Local Similarity	28.1%	Pred. No. 2.1e-14;		
Matches 119;	Conservative 62;	Mismatches 153;	Indels 90;	Gaps 25;

Oy	18	FLLLS---	LCLDGQAK-EKFKTFLVFRHGR-GPIETFPDPIRESM---	POGFOL	69
Oy	19	---	---	---	---
Oy	20	---	---	---	---
Oy	21	---	---	---	---
Oy	22	---	---	---	---
Oy	23	---	---	---	---
Oy	24	---	---	---	---
Oy	25	---	---	---	---
Oy	26	---	---	---	---
Oy	27	---	---	---	---
Oy	28	---	---	---	---
Oy	29	---	---	---	---
Oy	30	---	---	---	---
Oy	31	---	---	---	---
Oy	32	---	---	---	---
Oy	33	---	---	---	---
Oy	34	---	---	---	---
Oy	35	---	---	---	---
Oy	36	---	---	---	---
Oy	37	---	---	---	---
Oy	38	---	---	---	---
Oy	39	---	---	---	---
Oy	40	---	---	---	---
Oy	41	---	---	---	---
Oy	42	---	---	---	---
Oy	43	---	---	---	---
Oy	44	---	---	---	---
Oy	45	---	---	---	---
Oy	46	---	---	---	---
Oy	47	---	---	---	---
Oy	48	---	---	---	---
Oy	49	---	---	---	---
Oy	50	---	---	---	---
Oy	51	---	---	---	---
Oy	52	---	---	---	---
Oy	53	---	---	---	---
Oy	54	---	---	---	---
Oy	55	---	---	---	---
Oy	56	---	---	---	---
Oy	57	---	---	---	---
Oy	58	---	---	---	---
Oy	59	---	---	---	---
Oy	60	---	---	---	---
Oy	61	---	---	---	---
Oy	62	---	---	---	---
Oy	63	---	---	---	---
Oy	64	---	---	---	---
Oy	65	---	---	---	---
Oy	66	---	---	---	---
Oy	67	---	---	---	---
Oy	68	---	---	---	---
Oy	69	---	---	---	---
Oy	70	---	---	---	---
Oy	71	---	---	---	---
Oy	72	---	---	---	---
Oy	73	---	---	---	---
Oy	74	---	---	---	---
Oy	75	---	---	---	---
Oy	76	---	---	---	---
Oy	77	---	---	---	---
Oy	78	---	---	---	---
Oy	79	---	---	---	---
Oy	80	---	---	---	---
Oy	81	---	---	---	---
Oy	82	---	---	---	---
Oy	83	---	---	---	---
Oy	84	---	---	---	---
Oy	85	---	---	---	---
Oy	86	---	---	---	---
Oy	87	---	---	---	---
Oy	88	---	---	---	---
Oy	89	---	---	---	---
Oy	90	---	---	---	---
Oy	91	---	---	---	---
Oy	92	---	---	---	---
Oy	93	---	---	---	---
Oy	94	---	---	---	---
Oy	95	---	---	---	---
Oy	96	---	---	---	---
Oy	97	---	---	---	---
Oy	98	---	---	---	---
Oy	99	---	---	---	---
Oy	100	---	---	---	---

RESULT 15  
T16058  
hypothetical protein F13D11.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text-change 23-Mar-2001  
C:Accession: T16058  
R:Fulton, L.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of *C. elegans* cosmid F13D11.  
A:Reference number: S69020  
A:Accession: T16058  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-416 <FNU>  
A:Cross-references: EMBL:U04939; NID:g1072175; PID:g1072178; PIDW:AAA81702.1; CESP:FT  
C:Genetics:  
A:Gene: CESP:F13D11.1  
A:Introns: 23/3; 59/3; 86/3; 138/3; 202/3; 244/1; 270/3; 312/3; 349/3; 377/1  
C:Superfamily: mammalian acid phosphatase





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 2, 2001, 18:13:51 ; Search time 22.77 Seconds

(without alignments)  
1025.043 Million cell updates/sec

Title: US-09-402-845-2

Perfect score: 2060

Sequence: 1 MGAVPPLPSFTASLSGLFL.....DMATECMATSSHQCTVAGLG 385

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq.0601.\*

1:	/SID58/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID58/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID58/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID58/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID58/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID58/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID58/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID58/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID58/gcgdata/geneseq/geneseq/AA1989.DAT.*
11:	/SID58/gcgdata/geneseq/geneseq/AA1990.DAT.*
12:	/SID58/gcgdata/geneseq/geneseq/AA1991.DAT.*
13:	/SID58/gcgdata/geneseq/geneseq/AA1992.DAT.*
14:	/SID58/gcgdata/geneseq/geneseq/AA1993.DAT.*
15:	/SID58/gcgdata/geneseq/geneseq/AA1994.DAT.*
16:	/SID58/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID58/gcgdata/geneseq/geneseq/AA1996.DAT.*
18:	/SID58/gcgdata/geneseq/geneseq/AA1997.DAT.*
19:	/SID58/gcgdata/geneseq/geneseq/AA1998.DAT.*
20:	/SID58/gcgdata/geneseq/geneseq/AA1999.DAT.*
21:	/SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2060	100.0	385	20	AAW30574
2	1661.5	80.7	386	20	AAW57418
3	1661.5	80.7	386	20	AAW59081
4	1661.5	80.7	386	21	AAW59293
5	1661.5	80.7	515	18	AAW19762
6	939	45.6	216	21	AAW56451
7	880.5	42.7	210	21	AAW00216
8	689.5	33.5	178	21	AAW00217
9	689.5	33.5	171	21	AAW56447
10	315.5	15.3	421	21	AAW09699
11	315.5	15.3	428	20	AAW13368

12	315.5	15.3	428	21	AAW24399	Human PRO231 prote
13	313.5	15.2	428	22	AAW80236	Human PRO231 prote
14	260.5	12.6	106	21	AAW03770	Human secreted pro
15	208.5	10.1	480	20	AAW41742	Human PRO706 prote
16	208.5	10.1	480	21	AAW44298	Human PRO706 (UNQ3
17	208.5	10.1	480	22	AAW87346	Human gene 5 encod
18	175	8.5	519	22	AAW31601	Amino acid sequenc
19	169	8.2	468	21	AAW30243	Arabidopsis thalia
20	164.5	8.0	398	17	AAW94685	Flea salivary protei
21	154	7.5	31	20	AAW30575	Mouse prostatic ac
22	153.5	7.5	141	22	AAW20323	Human protein phos
23	151.5	7.4	353	18	AAW30484	Flea salivary protei
24	150.5	7.3	353	18	AAW82374	Flea salivary protei
25	147.5	7.2	524	22	AAW31600	Amino acid sequenc
26	144.5	7.0	375	19	AAW82382	Flea salivary protei
27	139	6.7	356	19	AAW82384	Flea salivary protei
28	135	6.6	355	19	AAW82385	Flea salivary protei
29	122	5.9	446	21	AAW31598	Amino acid sequenc
30	121.5	5.9	440	21	AAW20501	Aspergillus terren
31	121.5	5.9	440	21	AAW69544	A. terreus phytase
32	121.5	5.9	466	20	AAW39897	Phytase protein.
33	121.5	5.9	467	17	AAW88618	Flea salivary protei
34	117.5	5.7	153	17	AAW94683	Thermomyces lanugi
35	114.5	5.6	440	21	AAW20522	Thermomyces lanugi
36	114.5	5.6	440	21	AAW69564	Thermomyces lanugi
37	114.5	5.6	475	18	AAW27384	Thermomyces lanugi
38	114.5	5.6	475	18	AAW35724	T. lanuginosus CBS
39	114.5	5.6	475	20	AAW39898	Thermomyces phy
40	114.5	5.6	475	20	AAW94306	Thermomyces lanugi
41	113.5	5.5	467	20	AAW43170	Consensus phytase-
42	113.5	5.5	467	21	AAW20527	Consensus phytase
43	113.5	5.5	467	21	AAW69569	Mutant phytase-10,
44	112.5	5.5	467	21	AAW20534	Consensus phytase
45	112.5	5.5	489	22	AAW71729	P.hordei phytase p

## ALIGNMENTS

RESULT 1					
ID	AAW30574	standard; Protein: 385 AA.			
AC	AAW30574;				
DT	01-MAR-1999	(first entry)			
DE	Mouse prostatic acid phosphatase.				
KW	Prostatic acid phosphatase; PAP; mouse; tumour related antigen;				
XX	diagnosis; vaccine.				
OS	Mus sp.				
FH	Key	Location/Qualifiers			
FT	Peptide	1..31 /label= Sig_peptide			
FT	Misc-difference 364	/note="encoded by CCB"			
XX					
PN	WO9846769-A1.				
PD	22-OCT-1998.				
XX					
PF	10-APR-1998;	98WO-US07232.			
XX					
PR	11-APR-1997;	97US-0043301.			
XX					
PA	(DEND-) DENDREON CORP.				
XX					
PI	Laus R, Ruegg CL, Shapero MH, Yang D;				
XX					
DR	WPI, 1999-009335/01.				

DR N-PSDB: AAV45592.  
XX New mouse prostatic acid phosphatase - used to induce an immune  
PT response against tumour related antigens  
XX  
PS Claim 1; Page 20-21; 30pp; English.  
XX  
CC This is the amino acid sequence of mouse prostatic acid phosphatase  
CC (PAP), a novel tumour associated antigen. PAP cDNA (see AAV45592)  
CC was cloned from mouse prostate organ cDNA, and can be used in the  
CC recombinant production of mouse PAP. A method for producing an  
CC immune response against an autologous polypeptide tumour antigen  
CC (e.g. human PAP) involves immunising a subject with a xenogeneic  
CC antigen (e.g. mouse PAP), either alone, as part of a viral antigen  
CC construct, or as part of a pulsed dendritic cell preparation.  
CC Recombinant viruses expressing PAP are used in compositions to  
CC elicit immune responses against a tumour related antigen. The  
CC compositions are also useful for reducing tumour cell load.  
XX  
SQ Sequence 385 AA;

Query Match Best Local Similarity 100.0%; Score 2060; DB 20; Length 385;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAVPLPLSPYASLSIGFLLLSLCLDPGQAKELKFTLVFRHGRGPIETFPDPTES 60  
DB 1 mgavplplspyaaslsigfllllslcldpqgakelkftlvfrhgrdrgliefpdpptes 60  
QY 61 SSWPGFQGLTQWGMEOHKEGYSYRKRYGRFLNDTYKHDQIYIRSTVDRLMSAMTNA 120  
DB 61 swpgfsgqltqwgmeqhyelsgyirkygrflndtykhdqiyirstdvdrllmsamtnla 120  
QY 121 ALFPEEGISINNPRLMQPIPVHTVSLSEDRLLYLPFDCRPFEEELKSETLESEEFLLKRL 180  
DB 121 alfppegislnnpriqlwqpihvhtvslsedrlllylprfdrpfelksetleseeefllkrl 180  
QY 181 HPYKSFLLDTLSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPSWATDAMIKEISEL 240  
DB 181 hpyksflldtlsslsqfddqdlfgilwskvydplfcsvhnftlpswatedamkikeisel 240  
QY 241 SLSLSYGIHKKKESRLOGGVLVNEILKNMGLATOPKRYKLVMSAHDITVSGIOMALD 300  
DB 241 slslsygihkksrloggvlnvneilknmklatopqkykklvmsahdtvsglqmald 300  
QY 301 VYNGVLPYASCHMMELXHDKGHFVEMYRYNETQNEPYPLTLPGCTHSCPLEKFAELLD 360  
DB 301 vyngvlpypaschmmelyhdkghfvemyrynetqnepypltlpgcthscplekfaellld 360  
QY 361 PVIPQDMATECMATSSHQTVGALG 385  
DB 361 pvipqdwatecmatsshqtvgalg 385

RESULT 2  
AAW57418 ID AAW57418 standard; Protein: 386 AA.  
XX  
AC AAW57418;  
XX  
DT 07-AUG-1998 (first entry)  
XX  
DE Protein encoded by a human prostate cancer marker.  
XX  
KM Prostate cancer; human; marker; diagnosis; treatment; probe.  
XX  
OS Homo sapiens.  
XX  
PN WO9804689-A1.  
XX  
PD 05-FEB-1998.  
XX

PF 31-JUL-1996; 96WO-US12516.  
XX  
PR 31-JUL-1996; 96WO-US12516.  
XX  
PA (UROC-) UROCOR INC.  
XX  
PI An G, O'hara SM, Ralph D, Veltri R;  
XX  
DR WPI: 1998-130681/12.  
XX  
DR N-PSDB: AAV29653.  
XX  
PT Human prostate cancer marker - useful for detection and treatment of  
PT human prostate cancer  
XX  
PS Disclosure; Pages 167-174; 229pp; English.

CC This protein is encoded by a marker sequence for human prostate cancer.  
CC Isolated nucleic acid segments shown in AAV16881 to AAV16885, AAV16890  
CC to AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer  
CC markers are provided in the specification. It also provides methods for  
CC identifying markers for human prostate cancer and for detection of  
CC prostate cancer cells. The markers can be identified by amplifying human  
CC prostate RNA to provide nucleic acid amplification products, separating  
CC the products and identifying those RNA that are differentially expressed  
CC between human prostate cancers versus normal or benign human prostate.  
CC Prostate cancer cells in a sample can be detected by detecting a nucleic  
CC acid in a sample, the nucleic acid being a prostate cancer marker.  
CC Probes and primers derived from this marker can be used for the detection  
CC of prostate cancer cells in a sample. Antibodies against the protein  
CC encoded by the marker nucleic acid fragments, inhibitors of the protein  
CC and oligonucleotides antisense to the markers can be used in the  
CC treatment of prostate cancer. The antibodies can also be used for the  
CC diagnosis of human prostate cancer.  
XX  
SQ Sequence 386 AA;

Query Match Best Local Similarity 80.7%; Score 1661.5; DB 19; Length 386;  
Matches 311; Conservative 26; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGAVPLPLSPYASLSIGFLLLSLCLDPG-QAKELKFTLVFRHGRGPIETFPDPTTE 59  
DB 1 mraaplllraaaslsigfllflfwldrsvlakelkftlvfrhgrdspitdftdpdike 60  
QY 60 SSWPGFQGLTQWGMEOHKEGYSYRKRYGRFLNDTYKHDQIYIRSTVDRLMSAMTNA 119  
DB 61 swpgfsgqltqwgmeqhyelsgyirkygrflndtykhdqiyirstdvdrllmsamtnl 120  
QY 120 AALFPEEGISINNPRLMQPIPVHTVSLSEDRLLYLPFDCRPFEEELKSETLESEEFLLKRL 179  
DB 121 aalfppegislnnpriqlwqpihvhtvslsedrlllylprfdrpfelksetleseeefllkrl 180  
QY 180 LHPYKSFLLDTLSSLSGFDQDLFGIMSKVYDPLFCESVHNFTLPSWATDAMIKEISEL 239  
DB 181 lhpysflldtlsslsqfddqdlfgilwskvydplfcsvhnftlpswatedamkikeisel 240  
QY 240 SLSLSYGIHKKKESRLOGGVLVNEILKNMGLATOPKRYKLVMSAHDITVSGIOMALD 299  
DB 241 slslsygihkksrloggvlnvneilknmklatopqkykklvmsahdtvsglqmal 300  
QY 300 VYNGVLPYASCHMMELXHDKGHFVEMYRYNETQNEPYPLTLPGCTHSCPLEKFAELLD 359  
DB 301 dyngvlpypaschmmelyhdkghfvemyrynetqnepypltlpgcthscplekfaellld 360  
QY 360 DVIPTQDMATECMATSSHQGT 380  
DB 361 gviptqdwatecmatsshqgt 381

RESULT 3  
AAW95081 ID AAW95081 standard; Protein: 386 AA.

```

XX AA095081;
AC 20-MAR-1999 (first entry)
XX Protein sequence Seq ID No: 47 from US 5882864.
DE
XX
XX Prostate cancer; benign prostatic hyperplasia; marker gene; tumour;
KM differentiation; Reverse Transcription Polymerase Chain Reaction;
KM diagnostic; progression; cancer; metastasis; RT-PCR.
XX
XX Homo sapiens.
OS
XX US5882864-A.
XX 16-MAR-1999.
XX
XX 31-JUL-1996; 96US-0692787.
XX
XX 31-JUL-1995; 95US-0001655.
XX 31-JUL-1996; 96US-0692787.
XX (UROC-) UROCOR INC.
XX
XX An G, O'Hara SM, Ralph D, Veltri R;
XX
XX WPI: 1999-214055/18.
XX N-PSDB: AAX26062.
XX
XX Diagnosing prostate cancer and benign prostatic hyperplasia cells
XX using oligonucleotide probes specific for marker genes associated
XX with tumor differentiation and progression in Reverse Transcription
XX Polymerase Chain Reaction analysis
XX
XX Disclosure: Column 93-98; 74pp; English.
XX
XX The invention relates to methods for diagnosing prostate cancer or benign
XX prostatic hyperplasia cells in a biological sample. The method uses
XX oligonucleotides specific for marker genes associated with tumour
XX differentiation and progression in Reverse Transcription Polymerase Chain
XX Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful
XX for detecting and monitoring the progression of benign prostatic
XX hyperplasia and human prostate cancer (the most prevalent form of cancer
XX and a major cause of death in males) prior to the tumor undergoing
XX metastasis, therefore allowing the optimal method of treatment to be
XX determined before the condition becomes life threatening.
XX
XX Sequence 386 AA:
SQ

```

```

OY 300 DYNNGVLPYASCHMELVHDKGHFVEMYRNETONEPYPLTLPCTHSCPLEKFAELL 359
DB 301 dyngllppaschlelyekgeyivemyrnetqhepylmlpgcspclleaeiv 360
OY 360 DVIYPODMATECMATSSHOQT 380
DB 361 gviydpqdwsteclntshqgt 381

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RESULT 4  
AA59293  
ID AA59293 standard; peptide; 386 AA.  
XX  
AC AA59293;  
XX  
DT 19-APR-2000 (first entry)  
XX  
DE Prostatic acid phosphatase marker UC Band #47 amino acid sequence.  
XX  
KM Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer;  
KM benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection.  
XX  
OS Homo sapiens.  
XX  
PN WO964631-A1.  
XX  
PD 16-DEC-1999.  
XX  
PF 11-JUN-1999; 99WO-US13151.  
XX  
PR 12-JUN-1998; 98US-0097199.  
XX  
PA (UROC-) UROCOR INC.  
XX  
PI An G, O'Hara SM, Ralph D, Veltri RW;  
XX  
DR WPI: 2000-116557/10.  
DR N-PSDB: AA287547.  
XX  
PT Novel RNA biomarkers for diagnosis, prognosis and management of  
PT prostate, breast and bladder cancer  
XX  
PS Example 2; Page 173-176; 191pp; English.  
XX  
XX The invention provides nucleic acid markers of prostate, breast and  
XX bladder cancer. The markers are indicators of malignant transformation of  
XX prostate, breast and bladder tissues and are diagnostic of the potential  
XX for metastatic spread of malignant prostate tumours. The nucleic acid can  
XX also be used as targets for therapeutic intervention in prostate cancer,  
XX benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The  
XX markers may be used to design specific probes and primers, for the rapid  
XX analysis of prostate, bladder or breast biopsy samples. The probes and  
XX primers may also be used for in situ hybridization or in situ PCR  
XX detection and diagnosis. They may also be used to identify and isolate  
XX full length gene sequences from various DNA libraries. Antibodies  
XX against the polypeptide products of the markers can be used to treat  
XX prostate cancer, bladder cancer or breast cancer. The encoded proteins  
XX may be used to detect antibodies. The proteins and antibodies can be  
XX used in immunodetection methods for detecting or quantifying the cancers,  
XX and for clinical diagnosis of these cancers. The antibodies may also be  
XX used for radioimaging to quantify and localize the encoded proteins.  
XX  
XX Sequence 386 AA:  
SQ

Query Match 80.7%; Score 1661.5; DB 21; Length 386;  
Best Local Similarity 81.6%; Pred. No. 1.9e-156;  
Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

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OY 1 MGAIVPLSPFTASISGFLLLSLCLDPPG-OAKELKFTLVPRHGRPIETPTDPIITE 59
DB 1 mraaplllaraaslsigfllflfwldrsvlaelkfvltvfrhgrspdtptdpikpe 60
OY 60 SSMPOFGOLTQWGMQDHYELSGYIRKRYGRFLNDTYKHDQYIRSTDVRTLMSAMTNL 119
DB 61 sswpgdfigltqgmeghyelgyirkyrkfinesykhgyirstdvdrtlmsamtnl 120
OY 120 AALFPEEGISINNPRLMOPIPYHYVLSLSDRLLYLPFRDCPFEEELKSTLESEFLKR 179
DB 121 aalfppegyslwnpdlwqplpvtvplsedqlllylfrncprfgelesetlkseeffqxr 180
OY 180 LHPYKSLFDTLSLSGFDODLFGIMSKYVDPPLFCESVHNFTLPPSNATEDAMIKLELISE 239
DB 181 lhpkykfaictlqklsghqdlfigvskvydpdycesvhnftlpsvatedamkkllelse 240
OY 240 LSLSLYGIHKOKESKRSLOGVLVNELKLNKMLATOPORYYKKILVMYSAHDTYVSGLOMAL 299
DB 241 lslslsygihkqekerslqgyvlvnelnhmkratqipyskklmlysahtdtvsglqmal 300

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0y 60 SSMPOGFEQULQOMGMEQHYELGASTIRKRYGAFELNDTYKHOQIYIRSTDVRTLMSAVTNL 119
Db 61 sswpgqfsgqltqlmeqhyelgeyirkyrykrlfinesykeqvyirstdvtrtlmsamtal 120
0y 120 AALPPEEISTIMNRRILMQPPIVHTVLSLSEBRLLYLPRFRCOPREELKSTLESEEFIR 179
Db 121 aalfppegvstwnprlllwqrpivhtvpsedqilylrpfrncprlqeeletlseeqkr 180
0y 180 LHPYSEFLDTLSLSGFDQDDELGFIMSKVYDPLFCESVHNHFTPLSPMATEAMIKELSE 239
Db 181 lhpkydfiatrlgkrsqhlngdqlfglswkyvdrplyrcevhftlpswatetmtkklrelse 240
0y 240 LSLSLVGIHOKESKRLQSGCVLVEINELIKNNKATLQPOKYKKLWMTSAHDTVSGIOMAL 299
Db 241 lslslsygihbkqeksrtdqgsvlveinelnhmkkratqtpgkklmwsahadtvtsgjmal 300
0y 300 DYKNCVLPYPYASCHMMEIYHDKGHEFVEMTYRNETQNEPRPLPLPGCTSHCPLEKRADELL 359
Db 301 dvyngllppryaschltelyfeykgeyfemymrnetqheprlmipgspescpierfaelay 360
0y 360 DVPIDODMATECMATSSHOGF 360
Db 361 gvpipqdwstecmtcnsngqt 361

```

## RESULT 5

ID AAW19762 standard; Protein; 515 AA.

AAW19762;

DT 17-SEP-1997 (first entry)

PAP-GM-CSF immunostimulatory fusion protein.

PAP-GM-CSF; granulocyte macrophage colony stimulating factor;

**KW** Immunostimulant; prostate cancer; immunisation; therapy.

OS Homo sapiens.

**FH Key**

ET

Protein FT

ET :

PROCED  
ET

republic  
ET

Protein

FT Disaffidation

FT Disulfide-bor  
FT Disulfide-bor

ET Disulfide-bond

Modified-site  
ET

ET  
ET  
MOT + 4102  
+ 0

FF

FT Modified-site

ET  
DE

ET

Oy	60	SSMPOGFEQLTQMGMEQHNYELGASTIRKRYGFLEMDTYKKHQDIYTRSDVDRTLMSATNL	119
Db	61	sswpqifqlclqlmeqhyelgyrlrkyrkflnesykhqvylrstdvdrclmsamtnl	120
Oy	120	AALFPEGISITMNPRLMQPVPHTVSLSEEDRLILYLPFDCPREELKSTLESEFLIKR	179
Db	121	aalfpepvstlwnp1llwqplvptlvp1seqdllylprncprlqescllseeqlkr	180
Oy	180	LHPYKSFLDLTLSLSEGFDDDLDFGIRSKVYDPLFCESVSNHFTLPSPWATEDAMIKLELSE	239
Db	181	lhpykdfatlatgkislghlqglfglswkvypdyplseesvnmfltpswatetmklrelse	240
Oy	240	LSLSLSYIHHOKESKRIGQGVLYNELIKNMKLATPQKTKKLLVMSAHDTVSGIQMAL	299
Db	241	ls1slsy1ghbqkexsr1ggv1vne1lnmkrcatqipsykk1lmyshahdtvsg1qmal	300
Oy	300	DVYNGVLPBPYKSCMHMELIYHDKGFHEMYRYNRTQNEPRPLTLPGCTHSCPLERKAELL	359
Db	301	dvynqgl1ppypaschltelylekgyfemyyrnetqhepylnlpgcspcpleriaelv	360
Oy	360	DPVIRPDWATECMATSSHQGT 380	
Db	361	gpvlipqdkwsteemtlnshqgt 381	
RESULT	5		
AA19762			
ID	AA19762	standard; Protein: 515 AA.	
XX	AA19762:		
XX	17-SEP-1997	(first entry)	
DE	PAP-GM-CSF	Immunostimulatory fusion protein.	
XX			
KM	PAP-GM-CSF;	granulocyte macrophage colony stimulating factor;	
KW	prostatic acid phosphatase; tumour-specific antigen;		
XX	immunostimulant; prostate cancer; immunisation; therapy.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FH	Peptide	1..32	
FT		/label= "Sig-peptide	
FT		/note= "PAP signal peptide"	
FT	Protein	33..515	
FT		/label= "M1-protein	
FT	Protein	/note= "PAP-GM-CSF fusion"	
FT		33..386	
FT	Peptide	/label= "PAP	
FT		387..388	
FT	Protein	/label= "linker	
FT		/note= "product of BamHI linker"	
FT		389..515	
FT	Protein	/label= "GM-CSF	
FT		161..372	
FT	Disulfide-bond	215..313	
FT	Disulfide-bond	347..351	
FT	Disulfide-bond	442..484	
FT	Disulfide-bond	476..509	
FT	Modified-site	94	
FT		/label= "Glycosylation	
FT		/note= "potential N-glycosylation site"	
FT	Modified-site	220	
FT		/label= "Glycosylation	
FT	Modified-site	333	
FT		/label= "Glycosylation	
FT		/note= "potential N-glycosylation site"	
FT	Modified-site	415	
FT		/label= "Glycosylation	
FT		/note= "potential N-glycosylation site"	

FT	Modified-site	425
FT	/label= Glycosylation	
XX	/note= "potential N-glycosylation site"	
XX		
PN	M09724438-A1.	
XX		
PD	10-JUL-1997.	
XX		
PF	23-DEC-1996;	96WO-U520241.
XX		
PR	28-DEC-1995;	95US-O579823.
XX		
PA	(ACTI-) ACTIVATED CELL THERAPY INC.	
XX		
PI	Laus R, Ruegg CL, Wu H;	
XX		
DR	WPI: 1997-363674/33.	
DR	N-PADB: AAT72721.	
XX		
PT	Potent APC that activates T-cells to give multivalent cellular	
PT	immune response - can also induce a cytotoxic T-cell response in a	
PT	vertebrate subject	
XX		
PS	Example 1; Fig 2; 45pp: English.	
XX		
CC	A fusion protein (AAW19762) comprises human prostatic acid	
CC	phosphatase (PAP, a tumour-specific antigen) and granulocyte-	
CC	macrophage colony stimulating factor (GM-CSF). It is the	
CC	expression product of a nucleic acid molecule (AAT72721) prepd. by	
CC	PCR amplification of PAP GM-CSF cDNAs and their fusion via a BamHI	
CC	linker. Fusion expression vectors can be used to transfect	
CC	mammalian and insect cells. The PAP-GM-CSF fusion protein is used	
CC	to induce anti-PAP immunity. The PAP-GM-CSF fusion protein is used	
CC	cytotoxic T lymphocytes (CTL) and as a target for prostate cancer	
CC	cells when combined with the dendritic cell binding protein GM-CSF	
CC	and used to stimulate antigen presenting cells that are then used	
CC	to prime CTL.	
XX		
IQ	Sequence	515 AA;

Query Match	80.78; Score 1661.5; DB 18; Length 515;
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Matches 311; Conservative 28; Mismatches 41; Indels 1; Gaps 1;

1 MGAVPLPLSP<sup>1</sup>TASLSLG<sup>2</sup>FL<sup>3</sup>LL<sup>4</sup>SL<sup>5</sup>CL<sup>6</sup>DPG-QAKELK<sup>7</sup>VT<sup>8</sup>L<sup>9</sup>VERH<sup>10</sup>GDRG<sup>11</sup>PIET<sup>12</sup>FP<sup>13</sup>TP<sup>14</sup>ITE 59

1 mraaplllaraaslsqflflffwldrsvlakelkfvtlvfrhqdrspidttfptdpik 60

60 SSWPQGGOLTOWGMEOHYELGSYIRKRYGFLNDTYKHDOYIRSTVDVDTLMSAMTNL 119

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61 sswbaafaa]ta]ameahve]evrkrvrf]nesvkheuv]rstdydr]msamtn) 120
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120 AALEPPEGISIWNPRIJWOPIPVHTVSI.SEDRI.I.YI.PFRDCPRFEET.KSETI.ESEEEI.KR 179

121 aa] f n n e v s i w n o f l ] w a n f n v h t v n l s e d a l ] v ] n f n c n r f c a l e e s e t l k e e e f a k r 180

180 I.HPVKSEI DTI.SI.SGEDDODI.ECISKRVYDPI.ECESVHNNETI.DSWATEDAMIKI.KFI.SE.2399

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240 TESTICULAR VOLUME AND WEIGHT IN THE MALE RAT

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200 DIVERSITY AND COMMUNITY STRUCTURE

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[illegible]

RESULT 6  
ID AAB56451 standard; Protein: 216 AA.  
AC AAB56451;  
XX  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Human prostate cancer antigen protein sequence SEQ ID NO:1029.  
XX  
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
XX neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;  
XX vunerary; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;  
XX antibacterial; gene therapy; neural; immune; reproductive; renal;  
XX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
XX wound; infectious disease.  
XX  
XX Homo sapiens.  
XX  
XX WO20005174-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 08-MAR-2000; 2000MO-US05988.  
XX  
XX 12-MAR-1999; 99US-0124270.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
XX  
XX Rosen CA, Ruben SM;  
XX  
XX WPI: 2000-587513/55.  
XX  
XX N-PSDB: AAF15654.  
XX  
XX  
XX Prostate cancer associated gene sequences, referred to as prostate  
XX cancer antigens, useful for treatment, prevention, and diagnosis of  
XX disorders such as prostate cancer -  
XX  
XX  
XX Claim 11; Page 1458-1459; 2338pp; English.  
XX  
XX AAF1566 to AAF1605 encode the human prostate cancer associated  
XX proteins, called prostate cancer antigens, given in AAB5663 to AAB57302.  
XX The prostate cancer antigens can have neuroprotective, cytosolic,  
XX cardioactive, immunomodulatory, muscular, vunerary, gastrointestinal,  
XX nephrotoxic, antineoplastic, gynaecological and antibacterial activities,  
XX and can be used in gene therapy. The prostate cancer antigen  
XX polynucleotides may be used for detection of prostate cancer, chromosome  
XX identification, as chromosome markers, and for numerous other diagnostic  
XX or research purposes. The prostate cancer antigens may be used to treat  
XX disorders such as neural, immune, muscular, reproductive,  
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
XX disorders, wounds, and infectious diseases. AAF1606 to AAF1614 to  
XX AAB57303 represent sequences used in the exemplification of the present  
XX invention.  
XX  
XX  
XX Sequence 216 AA;  
SQ

Query Match 45.6%; Score 939; DB 21; Length 216;  
Best Local Similarity 82.0%; Pred. No. 4.5e-85;  
Matches 173; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 170 TSESEFLRLHPYKSLDTLSLSCGFDQDLFGIMSKYDPLFCSEVHFTLPWATED 229  
DB 1 tkseefqqrllpykfdictlglslhgqdlfgiwsxydplicyevnmftlpswated 60  
QY 230 AMIKKELSELSTLYGIHKQKESRLQGVLVNEIKNMKLATOPQKYYKLWMSAHD 289  
DB 61 tmtklrelselstlslslyghkqkexsrlqgvylvnelnhmkrtatpkykklmsahd 120  
QY 290 TTVSGIQMLADYNGVLPYASCHMMELVHDKGCHFEVEMYRNENEPRLPLPCTHS 349

DB 121 ttvsglqmaladyngllppryaschltelyfexgeyfvemyrneutghpylmlpccps 180  
QY 350 CPLEKFAELLDPYIPQDMATECMATSSHOGT 380  
DB 181 cpleraelvgvlpqdwstecmtlnshgt 211

RESULT 7  
ID AAG00216 standard; Protein: 210 AA.  
AC AAG00216;  
XX  
XX 06-OCT-2000 (first entry)  
XX  
XX Human secreted protein, SEQ ID NO: 4297.  
XX  
XX  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
XX gene therapy; chromosome mapping.  
XX  
XX Homo sapiens.  
XX  
XX EP1033401-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 21-FEB-2000; 2000EP-0200610.  
XX  
XX 26-FEB-1999; 99US-0122487.  
XX  
XX (GEST) GENSET.  
XX  
XX Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
XX WPI: 2000-500381/45.  
XX  
XX N-PSDB: AAC00222.  
XX  
XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
XX  
XX Claim 13; SEQ ID 4297; 71pp + CD-ROM; English.  
XX  
XX The present sequence is a polypeptide encoded by one of a large number  
XX of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
XX were prepared from total human RNAs or polyA+ RNAs derived from 30  
XX different tissues. EST sequences usually correspond mainly to the 3'  
XX untranslated region (UTR) of the mRNA because they are often obtained  
XX from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
XX isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
XX those cases where longer cDNA sequences have been obtained, the full 5'  
XX UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
XX ends and can therefore be used to obtain full length cDNAs and genomic  
XX DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
XX chromosome mapping procedures. They are used to obtain upstream  
XX regulatory sequences and to design expression and secretion vectors.  
XX  
XX  
XX Sequence 210 AA;  
SQ

Query Match 42.7%; Score 880.5; DB 21; Length 210;  
Best Local Similarity 80.0%; Pred. No. 2.8e-79;  
Matches 168; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY 1 MGAIVPLPSPTASTLSIGFLLLSLCLDPG-QAKELFVTLVFNHGRGPREPTPTITE 59  
DB 1 mraaplllaraaslsigflillfwldrsylakelfvclvtlrngsrpsdtpcpkive 60  
QY 60 SSWPQGFQQLTQGMQOHVELSGYIRRRYGRFLNDYKHKDQYIRSTDYDRTLMSANTN 119  
DB 61 sswpgfgqtlqtgmeghyelsgyirkryrkflineykhbeylirstdtdrtlmsamtl 120





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PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063355.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.

XX (GETH ) GENENTECH INC.
XX
XX
XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX WPI: 1999-229533/19.
XX N-PSDB: AAX52239.
XX
XX New isolated human genes and polypeptides used in, e.g. treatment of
XX gastrointestinal ulceration
XX
XX
XX Claim 12; Fig 52; 320pp; English.
XX
XX
XX AA113344-403 represent secreted and transmembrane human proteins.
XX The cDNA sequences are obtained from cDNA libraries, prepared from
XX fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
XX The encoded polypeptides have specific uses based on their homology to
XX known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
XX associated with the preservation and maintenance of gastrointestinal
XX mucosa and with the repair of acute and chronic mucosal lesions
XX (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
XX ulceration and congenital microvillus atrophy), skin diseases associated
XX with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
XX cancers such as lung squamous cell carcinoma of the vulva and gliomas),
XX potent effects on cell growth and development, diseases related to
XX growth or survival of nerve cells including Parkinson's disease,
XX Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
XX as a target for anti-tumor drugs. PRO533 may be used in the treatment
XX of Usher Syndrome or Atrophia areata; PRO269 can be used as an
XX anti-thrombotic agent; PRO287 polypeptides and portions may have
XX therapeutic applications in wound healing and tissue repair; PRO317 can
XX be used for treating problems of the kidney, uterus, endometrium, blood
XX vessels, or related tissue, e.g. in the heart of genital tract.
XX
XX
XX Sequence 428 AA:
XX
XX
XX Query Match 15.3%; Score 315.5; DB 20; Length 428;
XX Best Local Similarity 26.9%; Pred. No. 1.le-22;
XX Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;
XX
XX 16 LGFLLLSLCLD-----FEQAK-----ELKVTLVFRRGRGRLPETPTD-- 55
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 14 yvltslaycqlqrvtlaelaeqdaqcpvdtsllklmvgvfrfgragspklpbleq 73

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Qy	56	-----PIRESSM-----PGCF-----GQLTQMGMEQHY 78
Db	74	wvnpqllwvppqcfidyvtnlagpkyrpydsqyhetclkgmfagqclkvgmqmf 133
Qy	79	ELGSYIRKRYR---FLNDTYRKNDQYIRSTDVDRTLMSAMNLALF--PREGISINNP 133
Db	134	algetlnyvedrpfisptfngpveflstnlfmlestlclaglficqkeg----- 187
Qy	134	RLMOPRIVHTVLSIEDRLLYLPRDCCPREELKSETLSEEFRLKRLNPKSFLDTLSSL 193
Db	188	-----rlilht-deadsevlpryqsc---wsjrtgrtgrqnaqlqpsjisedlkkvndr 238
Qy	194	SGFDODDLFGTMSKVYUPLFCESYHNNTPLRSMTEDAMIKLESLSLSLSYGHNQ-K 252
Db	239	mgldssdcvudffl-lldnvaeeqhn--lpscpmlkrfarmlegavd--tsilylprkcdr 294
Qy	253	EKSRLQGC---VLVNELTKNMKLAPORQYKKLVWYSADHTTVSGLOMALDLYVNGVLP 308
Db	295	eslqmaaygrflhilesnllkamdsatapkrlrlylyaahdvtfprlmtlglfchkwpr 354
Qy	309	YASCHMELYN--DKSGHFVEMYRYNETQNERPYLTLR-GCTHS-CRLEKFAELDD--PV 362
Db	355	favdtlmeelyghleskewfvglyyhqkeg-----vprsgcdglprldmflnamsyvl 407
Qy	363	IPQDMATECMAT 374
Db	408	spekyhalcsqt 419
RESULT 12		
AAB24399		
ID	AAB24399 standard; Protein; 428 AA.	
XX	AAB24399;	
AC	07-NOV-2000 (first entry)	
DT	Human PRO231 protein sequence SEQ ID NO:56.	
DE	Human; PRO; promotion; inhibition; angiogenesis; atherosclerosis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;	
KW	angiogenic; proliferative; cardiac; cardiovascular; antithrombotic;	
KW	cyclostatic; gene therapy; vaccine.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200032221-A2.	
PN	08-JUN-2000.	
XX	30-NOV-1999; 99WO-US28313.	
XX	01-DEC-1998; 98WO-US25108.	
PR	16-DEC-1998; 98US-0112850.	
PR	12-JAN-1999; 99US-0115554.	
PR	08-MAR-1999; 99WO-US05028.	
PR	12-MAR-1999; 99US-0123957.	
PR	28-APR-1999; 99US-0134445.	
PR	14-MAY-1999; 99WO-US12252.	
PR	02-JUN-1999; 99US-0141037.	
PR	23-JUN-1999; 99US-0144758.	
PR	20-JUL-1999; 99US-0145698.	
PR	26-JUL-1999; 99US-0145698.	
PR	01-SEP-1999; 99WO-US20594.	
PR	08-SEP-1999; 99WO-US20594.	
PR	13-SEP-1999; 99WO-US20944.	
PR	15-SEP-1999; 99WO-US21547.	
PR	05-OCT-1999; 99WO-US23089.	
PR	29-OCT-1999; 99US-0162506.	
XX	(GETH ) GENENTECH INC.	



XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 PI Watanabe CK, Williams PM, Wood WT;  
 XX  
 DR WPI: 2000-412154/35.  
 XX N-PSDB: AAA77553.  
 PT Nucleic acids encoding PRO polypeptides useful for preventing,  
 PT diagnosing and treating disorders of cardiovascular, endothelial or  
 PT angiogenic disorders in mammals -  
 XX  
 PS Claim 72; Fig 24; 315pp; English.  
 XX  
 CC The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating disorders in mammals by  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PRO expression such as cardiovascular, endothelial or  
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 428 AA;

Query Match 15.3%; Score 315.5; DB 21; Length 428;  
 Best Local Similarity 26.9%; Pred. No. 1.1e-22;  
 Matches 116; Conservative 62; Mismatches 155; Indels 99; Gaps 20;

QY 16 LGFLLLSICLD-----PGQAK-----ELKFTLVGRGDRGPIETFPD-- 55  
 DB 14 vglvltslaycllqrrvalaelgeadgqcpvdrslklkkmqvvrfrgatsplkplpleeq 73  
 QY 56 -----PTTESSW-----PGGF-----GOLTOGMEOHY 78  
 DB 74 vewnpqllevpqtdqdytrtnlaagpkpyspdyqshettlkgmfaagtlkvqmqmf 133  
 QY 79 ELGSIYRKRYGR--FLNDTYKHQIYIRSTDVDRTLMSAMTALAFL--PPEGISITWNP 133  
 DB 134 algerlrknyvedlplspfrpgevfirfstnfrlnestrcllaglfqgcqeg----- 187  
 QY 134 RLMMQIIPVHTVSLSDRLLYLPRFCOPREFELKSETLESEFLKRLHPRKSLDTITSL 193  
 DB 188 ----pilhlt-deadsevllypnysc---wsrlrqrtrgrtqaslpqpsidklkvkdr 238  
 QY 194 SGFDDDDLFCIGMSKVYDPLFCESVHNFTLPWSMATEDAMIKLSELSLTVGIRKO-K 252  
 DB 239 mgldssdkvdffl-ildnvaagahn--lpscmklrfamiegravd-tslylilkedr 294  
 QY 253 EKSRLGG---VLVNEILKNMKLATQPKYKRLVMYSAHDTVSGLOMALDVYNGVLP 308  
 DB 295 eslgmavgpflhllsenllkmdsatapdkirklylaahdvrfplmltligfndkwp 354  
 QY 309 YASCHMELVH--DKGCHVPEMYRYMETQNEPRLPLP-GCTHS-CPLEKFAELDL--PV 362  
 DB 355 faudlmetlqnhskewtqvlyhyhkeg-----vprgcpdglcpldmflnamsvytl 407  
 QY 363 IPQDNATECMAT 374  
 DB 408 spekyhalcsqt 419

AC AAB80236;  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Human PRO231 protein.  
 XX  
 KW Human: PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;  
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;  
 KW antiangiogenic; vasotropic; antiaesthetic; antineumatic; cancer;  
 KW antiarthritic; antidiarrheal; antidiabetic; antitumor; diabetes;  
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 KW ischaemia; inflammation.  
 XX  
 OS Homo sapiens.  
 PN WO200104311-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 22-FEB-2000; 2000MO-US04414.  
 XX  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 08-SEP-1999; 99MO-US20594.  
 PR 13-SEP-1999; 99MO-US20944.  
 PR 15-SEP-1999; 99MO-US21090.  
 PR 15-SEP-1999; 99MO-US21547.  
 PR 05-OCT-1999; 99MO-US23089.  
 PR 29-NOV-1999; 99MO-US28214.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 20-DEC-1999; 99MO-US30999.  
 PR 05-JAN-2000; 99MO-US00219.  
 XX  
 PA (GENTH) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Flvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin J;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WT;  
 XX  
 DR WPI: 2001-081051/09.  
 DR N-PSDB: AAF72397.  
 XX  
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in  
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
 PT Alzheimer's disease) -  
 XX  
 PS Claim 1; Fig 52; 393pp; English.  
 XX  
 CC The present sequence is one of sixty one novel secreted and  
 CC transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
 CC parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding, angiogenesis, ischaemias such as coronary  
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,  
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and  
 CC diabetes and retinal disorders such as retinitis pigmentosum.  
 CC The PRO nucleic acids have applications in molecular biology, including  
 CC use as hybridization probes, and in chromosome and gene mapping.  
 XX  
 SQ Sequence 428 AA;

Query Match 15.2%; Score 313.5; DB 22; Length 428;  
 Best Local Similarity 26.4%; Pred. No. 1.8e-22;  
 Matches 114; Conservative 63; Mismatches 156; Indels 99; Gaps 19;



PR 01-APR-1998; 98US-0080327.  
PR 01-APR-1998; 98US-0080328.  
PR 01-APR-1998; 98US-0080333.  
PR 01-APR-1998; 98US-0080334.  
PR 08-APR-1998; 98US-0081049.  
PR 08-APR-1998; 98US-0081070.  
PR 08-APR-1998; 98US-0081071.  
PR 09-APR-1998; 98US-0081195.  
PR 09-APR-1998; 98US-0081203.  
PR 09-APR-1998; 98US-0081229.  
PR 15-APR-1998; 98US-0081817.  
PR 15-APR-1998; 98US-0081838.  
PR 15-APR-1998; 98US-0081952.  
PR 15-APR-1998; 98US-0081955.  
PR 21-APR-1998; 98US-0082568.  
PR 21-APR-1998; 98US-0082569.  
PR 22-APR-1998; 98US-0082700.  
PR 22-APR-1998; 98US-0082704.  
PR 23-APR-1998; 98US-0082804.  
PR 23-APR-1998; 98US-0082767.  
PR 23-APR-1998; 98US-0082796.  
PR 27-APR-1998; 98US-0083336.  
PR 28-APR-1998; 98US-0083322.  
PR 29-APR-1998; 98US-0083392.  
PR 29-APR-1998; 98US-0083495.  
PR 29-APR-1998; 98US-0083496.  
PR 29-APR-1998; 98US-0083500.  
PR 29-APR-1998; 98US-0083545.  
PR 29-APR-1998; 98US-0083554.  
PR 29-APR-1998; 98US-0083558.  
PR 29-APR-1998; 98US-0083559.  
PR 30-APR-1998; 98US-0083742.  
PR 05-MAY-1998; 98US-0084366.  
PR 06-MAY-1998; 98US-0084414.  
PR 07-MAY-1998; 98US-0084598.  
PR 07-MAY-1998; 98US-0084600.  
PR 07-MAY-1998; 98US-0084627.  
PR 07-MAY-1998; 98US-0084637.  
PR 07-MAY-1998; 98US-0084639.  
PR 07-MAY-1998; 98US-0084640.  
PR 07-MAY-1998; 98US-0084643.  
PR 13-MAY-1998; 98US-0085323.  
PR 13-MAY-1998; 98US-0085338.  
PR 13-MAY-1998; 98US-0085339.  
PR 15-MAY-1998; 98US-0085573.  
PR 15-MAY-1998; 98US-0085579.  
PR 15-MAY-1998; 98US-0085580.  
PR 15-MAY-1998; 98US-0085582.  
PR 15-MAY-1998; 98US-0085689.  
PR 15-MAY-1998; 98US-0085697.  
PR 15-MAY-1998; 98US-0085700.  
PR 15-MAY-1998; 98US-0085704.  
PR 18-MAY-1998; 98US-0086023.  
PR 22-MAY-1998; 98US-0086392.  
PR 22-MAY-1998; 98US-0086414.  
PR 22-MAY-1998; 98US-0086430.  
PR 22-MAY-1998; 98US-0086486.  
PR 28-MAY-1998; 98US-0087098.  
PR 28-MAY-1998; 98US-0087106.  
PR 28-MAY-1998; 98US-0087208.  
PR 30-JUL-1998; 98US-0094651.  
PR 11-SEP-1998; 98US-0100038.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX WPI; 1999-551358/46.  
DR N-PSDB; AA234217.  
XX  
PT New secreted and transmembrane polypeptides and their polynucleotides,

PR useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders -  
XX  
PS Claim 12; Fig 155; 530pp; English.  
XX  
CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as  
CC sources of probes, primers, for chromosome mapping, and for generation  
CC of antisense sequences. They can also be used to create transgenic  
CC animals. The proteins can be used to treat a variety of diseases and  
CC disorders, depending on their function. Diseases that may be treated  
CC include blood coagulation disorders, cancers and cellular adhesion  
CC disorders. They may also be used to raise antibodies. AA233891 to  
CC AA234338, and AA21685 to AA24174 represent polynucleotide and  
CC polypeptide sequence given in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 480 AA;  
  
Query Match 10.1%; Score 208.5; DB 20; Length 480;  
Best Local Similarity 19.8%; Pred. No. 5,7e-12;  
Matches 84; Conservative 62; Mismatches 127; Indels 151; Gaps 15;  
  
QY 33 ELKFTLVFRHGRGP----- 48  
DB 87 klsvshvflrhgdrlylvpkltkrpeidclvaarkpynkleafismksqsgasfes 146  
QY 49 ----IEFPDPTTESSWPGFCOLQWCMQEHVELGSYTRKRY---GRPLNDYTKHQI 101  
DB 147 plnslpynphlce-----mgeltqtvvqnlngqllrdlylkkhklpndwaadql 200  
QY 102 YIRSTDVDTLMSAMTNLAALPPEGISIWNPRLLQWPIPVHTVSUSEDRLLYLPRED-- 159  
DB 201 yletgtksrltqsglalyflpd-----fdwkl-----yfrhqp 236  
QY 160 -----CPRFEELKSTLESEERLKLHRYKSLDTLSSGPDQDGLGINSKY- 208  
DB 237 saifcsqscycp---vngylekeq--rrgy-----lltknsqlekygemaklv 282  
QY 209 -----YDPLFCESVHNFTLPSWATEDAMIKLELSLSTLSTYGIHKOREK-- 254  
DB 283 dypktqlraanpidsmchchvnsfp--ctnrgcvmefkvikthqledererrekl 340  
QY 255 ----SRLGGVLYNEILKNNKLATPQKYYKLYVSAHDTTVSGLOALDVYNGVLPYVA 310  
DB 341 yfgysllgahpnlngtigrmgrategrkeelfalysahdvltspalsalgsafrfpa 400  
QY 311 SCHMMEIYHDK---GGHFEVAMY-----RRETONREYPLTLPGCTHSCPLEKF 355  
DB 401 arllfwdgdkreksvshvllnygvdtlftsfcdqdhkkrspkm-----cplnl 452  
QY 356 AELL 359  
DB 453 vrfv 456

Search completed: August 2, 2001, 18:18:46  
Job time: 295 sec

Part of Article 34 Amendment  
or is this a different Amendment

a set of papers

For a set with the Amendment

Don't know

Attorney

Over

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 2, 2001, 18:18:51 ; Search time 24.19 seconds  
(without alignments)  
2105.723 Million cell updates/sec

Title: US-09-402-845-2  
Perfect score: 2060  
Sequence: 1 MGAVPLPLSPASLSGLFLL.....DWATECMATSSHQGTGALG 385

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_Organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_prodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2000	97.1	381	11 Q9QXH7	Q9qhx7 mus musculus
2	649	31.5	447	5 Q9U5U0	Q9u5u0 drosophila
3	649	31.5	447	5 Q9TVH9	Q9tvh9 drosophila
4	648	31.5	447	5 Q9U5U4	Q9u5u4 drosophila
5	648	31.5	447	5 Q9U5T9	Q9u5t9 drosophila
6	648	31.5	447	5 Q9U5T7	Q9u5t7 drosophila
7	647.5	31.4	447	5 Q9U5T8	Q9u5t8 drosophila
8	647	31.4	447	5 Q9U5U6	Q9u5u6 drosophila
9	646	31.4	447	5 Q9U5U1	Q9u5u1 drosophila
10	645	31.3	447	5 Q9U5T8	Q9u5t8 drosophila
11	645	31.3	447	5 Q9U5T5	Q9u5t5 drosophila
12	645	31.3	447	5 Q9U5T2	Q9u5t2 drosophila
13	645	31.3	447	5 Q9U5T1	Q9u5t1 drosophila
14	645	31.3	447	5 Q9TV17	Q9tv17 drosophila
15	645	31.3	447	5 Q9TVX2	Q9tvx2 drosophila
16	644	31.3	447	5 Q9U5V1	Q9u5v1 drosophila
17	644	31.3	447	5 Q9U5V0	Q9u5v0 drosophila
18	644	31.3	447	5 Q9U5U9	Q9u5u9 drosophila
19	644	31.3	447	5 Q9U5U2	Q9u5u2 drosophila

20	644	31.3	447	5	Q9TW53	Q9tw53 drosophila
21	644	31.3	447	5	Q9TW40	Q9tw40 drosophila
22	644	31.3	447	5	Q9TW19	Q9tw19 drosophila
23	643	31.2	447	5	Q9U5U7	Q9u5u7 drosophila
24	643	31.2	447	5	Q9U5U5	Q9u5u5 drosophila
25	643	31.2	447	5	Q9U5T6	Q9u5t6 drosophila
26	643	31.2	447	5	Q9U5T4	Q9u5t4 drosophila
27	643	31.2	447	5	Q9U5T3	Q9u5t3 drosophila
28	641	31.1	447	5	Q9U5U3	Q9u5u3 drosophila
29	640	31.1	447	5	Q9U186	Q9u186 drosophila
30	640	31.1	447	5	Q9U187	Q9u187 drosophila
31	639	31.0	447	5	Q9U5U1	Q9u5u1 drosophila
32	638	31.0	447	5	Q9U5T0	Q9u5t0 drosophila
33	638	31.0	447	5	Q9U5S8	Q9u5s8 drosophila
34	637	30.9	447	5	Q9U5S9	Q9u5s9 drosophila
35	632	30.7	447	5	Q9U5U8	Q9u5u8 drosophila
36	616	29.9	438	5	Q9VAD0	Q9vad0 drosophila
37	567	27.5	392	5	Q9VVZ9	Q9vvz9 drosophila
38	487	23.6	410	5	Q9VW00	Q9vw00 drosophila
39	487	23.6	440	5	Q17373	Q17373 caenorhabdi
40	480	23.3	366	5	Q22630	Q22630 caenorhabdi
41	479	23.3	376	5	P90949	P90949 caenorhabdi
42	476	23.1	412	5	Q9VW01	Q9vw01 drosophila
43	468	22.7	344	5	Q20662	Q20662 caenorhabdi
44	384.5	18.7	395	5	Q9VD68	Q9vd68 drosophila
45	375	18.2	449	5	Q19076	Q19076 caenorhabdi

ALIGNMENTS

RESULT 1					
Q9QXH7	Q9QXH7	PRELIMINARY;	PRT;	381	AA.
AC	Q9QXH7;				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)				
DE	PROSTATIC ACID PHOSPHATASE.				
OS	Mus musculus (Mouse)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Crew M.D., Chatta G.S., Borg C.D.;				
RT	"Sequence and expression of mouse prostatic acid phosphatase.";				
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF210243; AAF23171.1;				
DR	HSSP; P20646; IRPA.				
DR	InterPro: IPR000560;				
DR	Pfam: PF00328; acid_phosphat; 1.				
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.				
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.				
SQ	SEQUENCE 381 AA; 43689 MW; 60AD6919D77CB241 CRC64;				

Query Match 97.1%; Score 2000; DB 11; Length 381;  
Best Local Similarity 98.7%; Pred. No. 6.2e-159;  
Matches: 374; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY	1	MGAVPLPLSPASLSGLFLLSLCLDLP	GOAKELKFTVLVFRHGDRGP	PIETFFTPDPTES	60
Db	1	MRAVPLPLSPASLSGLFLLSLCLDLP	GOAKELKFTVLVFRHGDRGP	PIETFFTPDPTES	60
QY	61	SWQFGQLTQWQMEQHYELGSIYRKRYGRFLNDYTKHDIYIRSTVDVDTLMSAMTNLA	120		
Db	61	SWQFGQLTQWQMEQHYELGSIYRKRYGRFLNDYTKHDIYIRSTVDVDTLMSAMTNLA	120		
QY	121	ALPPEGISIWNPRLLMQPIPVHTVVS	EDRLLYLP	PRDCPRFEELKSETLESEEFKRL	180
Db	121	ALPPEGISIWNPRLLMQPIPVHTVVS	EDRLLYLP	PRDCPRFEELKSETLESEEFKRL	180

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Qy 181 HPKSFSLDTLSSGFDQDDLFGLWSKVYDPLFCESVHNFTLPSWATEDAMIKLKEISEL 240
Db 181 HPKSFSLDTLSSGFDQDDLFGLWSKVYDPLFCESVHNFTLPSWATEDAMIKLKEISEL 240
Qy 241 SLLSLYGIHKKOKSRLOGGVLVNEILKNMKLATQPKYKLVMSYSAHDTTVSGLOMALD 300
Db 241 SLLSLYGIHKKOKSRLOGGVLVNEILKNMKLATQPKYKLVMSYSAHDTTVSGLOMALD 300
Qy 301 YNGVLPPYASCHMWELVHDKGGHFVEMYRNQNEPYPPLTLPCTHSCPLEKFAELLD 360
Db 301 YNGVLPPYASCHMWELVHDKGGHFVEMYRNQNEPYPPLTLPCTHSCPLEKFAELLD 360
Qy 361 VPIPDWATECMATSSHQG 379
Db 361 VPIQDWATECMATSSHQG 379

RESULT 2
ID Q9U5U0 PRELIMINARY; PRT; 447 AA.
AC Q9U5U0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J34ST/054;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
RT inferred from nucleotide variation at the AcpH-1 gene region of
RT Drosophila subobscura.";
RL Genetics 153:871-889(1999).
DR EMBL; AJ389443; CAB55941.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 50998 MW; FB7CDB4E1EBE5840 CRC64;

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Query Match 31.5%; Score 649; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 4.8e-46;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

Qy 28 PGQAKELKFTLVFRHGDGRGPIETPDPITESS-WPQGFGLTQWGMQEHYELGSIYRK 86
Db 54 PG---ELKFAHIVFRHGDRTVPDPTDPPNNRKFPTWPGQGLTNLKGQHYELGKWLNR 110
Qy 87 RYGRFLNDTYKHDIYIRSTDVRTLSAMTNLAALPEGISIWNPRLLMQPIPVHTVS 146
Db 111 RYKSLGSRYNEDIFVQSTDVDRTLMSAQSDLAGLEPQGDGIWNPRIQPVVHTVP 170
Qy 147 LSEDRLLYLPDRCPREFELKSETLE-SEEFKLRLHPYKSFSLTLSSLSG-----FDQ 199
Db 171 EKDSILAAK-ASCPAY-DYELATLEASSEFQALYVRYRELLSYLTQNSGRVKSFDIAQ 228
Qy 200 DLFGIWSKVYDPLFCESVHNFTLPSWATEDAMIKLKEISELSLLSLYGIHKKOKSRLOG 259
Db 229 YL-----NNTLFIEKLYNMTLPWA--EKVYKKELTYVSNFAFSTATUTRSMARUKT 279
Qy 260 GVLVNEILK--NMKLATQPKYKLVMSYSAHDTTVSGLOMALDVYNGVLPYPYASCHMEL 317
Db 280 GPLKLDIFERDKNLNQKLPDRSLWIYSAHDTTIANVLNSLKFELHSPYACIMLEM 339
Qy 318 -YHDKGGHFVEMYRNQNEPYPPLTLPCTHSCPLEKFAELLDVPIPDWATEC----M 372
Db 340 RVDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPKTLVKLYQDVLPPVNNERECKRSTM 398

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Db 280 GPLKLDIFERDKNLNQKLPDRSLWIYSAHDTTIANVLNSLKFELHSPYACIMLEM 339
Qy 318 -YHDKGGHFVEMYRNQNEPYPPLTLPCTHSCPLEKFAELLDVPIPDWATEC----M 372
Db 340 RVDSNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPKTLVKLYQDVLPPVNNERECKRSTM 398
Qy 373 ATSSHQGTGVA 383
Db 399 MMTYEANLGA 409

RESULT 3
Q9TVH9
ID Q9TVH9 PRELIMINARY; PRT; 447 AA.
AC Q9TVH9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALST/054; AND J8ST/054;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
RT inferred from nucleotide variation at the AcpH-1 gene region of
RT Drosophila subobscura.";
RL Genetics 153:871-889(1999).
DR EMBL; AJ389447; CAB55945.1; -.
DR EMBL; AJ389446; CAB55944.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51040 MW; E1CCDB4E0FAF5851 CRC64;

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Query Match 31.5%; Score 649; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 4.8e-46;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

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Qy 373 ATSSHQGTGVA 383  
Db 399 MMTYEANLGA 409

## RESULT 4

Q9U504 ID Q9U504 PRELIMINARY; PRT; 447 AA.  
AC Q9U504  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
GN ACPH-1.  
OS Drosophila subobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J57ST/100;  
RX MEDLINE=99442390; PubMed=10511564;  
RA Navarro-Sabate A., Aguade M., Segarra C.;  
RT "The relationship between allozyme and chromosomal polymorphism  
inferred from nucleotide variation at the AcpH-1 gene region of  
Drosophila subobscura.";  
RL Genetics 153:871-889(1999).  
DR EMBL; AJ389437; CAB59935.1; -.  
DR HSP; P15309; 2HPA.  
DR FlyBase; FBgn0013885; Dsub\AcpH-1.  
DR InterPro; IPR000560; -.  
DR Pfam; PF00328; acid.phosphat; 2.  
DR PRODOM; PD003823; -1.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.  
SQ SEQUENCE 447 AA; 51049 MW; D3E545BFB1301859 CRC64;

Query Match 31.5%; Score 648; DB 5; Length 447;  
Best Local Similarity 39.1%; Pred. No. 5.8e-46;  
Matches 145; Conservative 67; Mismatches 129; Indels 30; Gaps 12;

Qy 28 PGQAKELKFTVLRHGDGRPIETFPDPTTSS-WPQFGQLTQWMEQHVELGSIK 86  
Db 54 PG---ELKFAHVIPIRHGDRTPVDPTDPWNNRKFPTGWLTLNKGQHYELGKWL 110  
Qy 87 RYGRFLNDYTKHDIYIRSTDVRTLSAMTALAALPPGEGISLWNPRLWPIPVHTVS 146  
Db 111 RYKSLGSRVTNEDIFVQSTDVRTLSAQSDLAGLYEPOGDDIWNPRIDWQPVVHTVP 170  
Qy 147 LSEDRLLYLPFRDCPRFEELKSETLESEEFKRLH-PYKSFDLTSLSG-----FDDQ 199  
Db 171 EKDDSIILAAK-ASCPAY-DYELATLEASSEFSLHVRRELLSYLTQNSGRLVKSFIDAQ 228  
Qy 200 DLFGWSKVYDPLFCESVHNFTLPSWATEDAMIKLSELSLSLYGIHKEKESRLQG 259  
Db 229 YL-----NNTLFIEKLYNNTLPVWA--EKVYGKELTYVSNFAFSTATFTSMARLKT 279  
Qy 260 GVLVNEILK--NMKLTAPQKYKLVMSAHDVTVSGQALDVYNGVLPYPYASCHMEL 317  
Db 280 GPLLKDFEFDKLNQLKPDRLSLWYSAHDTTIANVLSKLFELHSPYACIMLEM 339  
Qy 318 -YHDKGGHFVEMYRYNETQNEPYPLTLPCTHSCPLKFAELLDPIPODWATEC-----M 372  
Db 340 RVDDSNTPLVSVFYKNTTA-EPLPLDIPGGLSCPLATLVKLYQDVLVNWRECKRSTM 398  
Qy 373 ATSSHQGTGVA 383  
Db 399 MMTYEANLGA 409

Qy 373 ATSSHQGTGVA 383

Db 399 MMTYEANLGA 409

## RESULT 5

Q9U5T9 ID Q9U5T9 PRELIMINARY; PRT; 447 AA.  
AC Q9U5T9  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
GN ACPH-1.  
OS Drosophila subobscura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J61ST/054;  
RX MEDLINE=99442390; PubMed=10511564;  
RA Navarro-Sabate A., Aguade M., Segarra C.;  
RT "The relationship between allozyme and chromosomal polymorphism  
inferred from nucleotide variation at the AcpH-1 gene region of  
Drosophila subobscura.";  
RL Genetics 153:871-889(1999).  
DR EMBL; AJ389444; CAB59942.1; -.  
DR HSP; P20646; IRPA.  
DR FlyBase; FBgn0013885; Dsub\AcpH-1.  
DR InterPro; IPR000560; -.  
DR Pfam; PF00328; acid.phosphat; 2.  
DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.  
SQ SEQUENCE 447 AA; 51099 MW; 76CB6A4A35A8E4A7 CRC64;

Query Match 31.5%; Score 648; DB 5; Length 447;  
Best Local Similarity 39.6%; Pred. No. 5.8e-46;  
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

Qy 28 PGQAKELKFTVLRHGDGRPIETFPDPTTSS-WPQFGQLTQWMEQHVELGSIK 86  
Db 54 PG---ELKFAHVIPIRHGDRTPVDPTDPWNNRKFPTGWLTLNKGQHYELGKWL 110  
Qy 87 RYGRFLNDYTKHDIYIRSTDVRTLSAMTALAALPPGEGISLWNPRLWPIPVHTVS 146  
Db 111 RYKSLGSRVTNEDIFVQSTDVRTLSAQSDLAGLYEPOGDDIWNPRIDWQPVVHTVP 170  
Qy 147 LSEDRLLYLPFRDCPRFEELKSETLE-SEEFKRLHYPKSFDLTSLSG-----FDDQ 199  
Db 171 EKDDSIILAAK-ASCPAY-DYELATLEASSEFSLHVRRELLSYLTQNSGRLVKSFIDAQ 228  
Qy 200 DLFGWSKVYDPLFCESVHNFTLPSWATEDAMIKLSELSLSLYGIHKEKESRLQG 259  
Db 229 YL-----NNTLFIEKLYNNTLPVWA--EKVYGKELTYVSNFAFSTATFTSMARLKT 279  
Qy 260 GVLVNEILK--NMKLTAPQKYKLVMSAHDVTVSGQALDVYNGVLPYPYASCHMEL 317  
Db 280 GPLLKDFEFDKLNQLKPDRLSLWYSAHDTTIANVLSKLFELHSPYACIMLEM 339  
Qy 318 -YHDKGGHFVEMYRYNETQNEPYPLTLPCTHSCPLKFAELLDPIPODWATEC-----M 372  
Db 340 RVDDSNTPLVSVFYKNTTA-EPLPLDIPGGLSCPLATLVKLYQDVLVNWRECKRSTM 398  
Qy 373 ATSSHQGTGVA 383  
Db 399 MMTYEANLGA 409

## RESULT 6

Q9U5T7 ID Q9U5T7 PRELIMINARY; PRT; 447 AA.  
AC Q9U5T7

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A4ST/054;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozymes and chromosomal polymorphism
inferred from nucleotide variation at the AcpH-1 gene region of
Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL; AJ389448; CAB59946.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51088 MW; A80B027ACA8D9279 CRC64;

Query Match 31.5%; Score 648; DB 5; Length 447;
Best Local Similarity 39.6%; Pred. No. 5.8e-46;
Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

Qy 28 PQQAKELKVFVLVFRHGDRGPIETPTDITESS-WPQGFQLTQMGMEQHYELGSGYIRK 86
   || |||| :||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 54 PG---ELAFHVIHFRGDRTPVDYPTDPNRRKFWPTGWGQLTNLGKEQHYELGKWLNR 110
   || || || || || || || || || || || || || || || || || || || ||
Qy 87 RYGRFLNDYKHDOYIRSTVDRTLSAMTNLAALFPEGISINWRLLWQIPVHTVS 146
   || || || || || || || || || || || || || || || || || || || ||
Db 111 RYKSLGSRYNEDIFVOSTVDRTLSAQSLAGLYEPQGDIDWNRIDWQVPVHTVP 170
   || || || || || || || || || || || || || || || || || || || ||
Qy 147 LSEDRLLYLPFRDCPRFELKSETLE-SEEFKRLHPYKSFIDTSLSG-----FDQ 199
   : || || || || || || || || || || || || || || || || || || ||
Db 171 EKDDSILAAK-ASCPAY-DYELATLEASSEFOALVRYRELLSYLTQNSGRVLSFIDAQ 228
   : || || || || || || || || || || || || || || || || || || ||
Qy 200 DLFGTWSKYVDPLFCESVHNFTLPNSATEDAMIKUKELSELSSLXYGIHKQKSRLOQ 259
   | : || || || || || || || || || || || || || || || || || ||
Db 229 YL-----NNTLFTEKLYNMTLPVWA--EKVYGKELTYVSNFAFSIATETRSMARLKT 279
   : || || || || || || || || || || || || || || || || || || ||
Qy 260 GVLVNEILK--NMKLATOPKYKLVMSYSAHDTTVSGLMALDVYNGVLPYASCHMMEL 317
   || || || || || || || || || || || || || || || || || || || ||
Db 280 GPLLKDIFERFDKLNQNLKPDRLSWIYSAHDTTIANVLNSLKLFLHSPPYAACIMLEM 339
   || || || || || || || || || || || || || || || || || || || ||
Qy 318 -YHDKGGHFVEMYRYNETQNEPYTLPGCTHSCPLEKFAELLDPIQDWATEC----M 372
   || || || || || || || || || || || || || || || || || || || ||
Db 340 RYDSDNTPLVSFYKNTTA-EPLPLDIPGCGLSCLPLTLVKLYQDVLVFNWERECKRSTM 398
   : || || || || || || || || || || || || || || || || || || ||
Qy 373 ATSSHQGVTVGA 383
   : : ||
Db 399 MMTYEANLGA 409
   : : ||

RESULT 7
O97168 PRELIMINARY; PRT; 447 AA.
AC O97168;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila guanche (Fruit fly).
```

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OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7266;
RN [1]
RP SEQUENCE FROM N.A.
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The acid phosphatase-1 gene region in the Drosophila species of the
subobscura cluster."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18841; CAB38563.1; -.
DR HSSP; P15309; 2HPA.
DR FlyBase; FBgn0019218; Dgua\AcpH-1.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51073 MW; 1950B73D3C0C8005 CRC64;

Query Match 31.4%; Score 647.5; DB 5; Length 447;
Best Local Similarity 37.4%; Pred. No. 6.4e-46;
Matches 154; Conservative 66; Mismatches 137; Indels 55; Gaps 13;

Qy 12 ASLSLGLFLLLS-----LCLDPGQAKELKVFVLVFRHGDR 46
   || || || || || || || || || || || || || || || || || || || ||
Db 13 ALLVIGVLCLLSFGIGNAVHIPTVGSSEGETRPPPDQATLPG---ELKFAHVIHFRGDR 69
   || || || || || || || || || || || || || || || || || || || ||
Qy 47 GPIETFTPTDITESS-WPQGFQLTQMGMEQHYELGSGYIRKRYGRFLNDYKHDOYIRS 105
   || || || || || || || || || || || || || || || || || || || ||
Db 70 TPVDYPTDPNRRKFWPTGWGQLTNLGKEQHYELGKWLNRKYSLLGSRVTNEDIFVQS 129
   || || || || || || || || || || || || || || || || || || || ||
Qy 106 TDVORTLSAMTNLAALFPEGISINWRLLWQIPVHTVSLEDRLLYLPFRDCPREE 165
   || || || || || || || || || || || || || || || || || || || ||
Db 130 TDVORTLSAQSLAGLYEPQGDIDWNRIDWQVPVHTVPEKDDSILAAK-ASCPAY-D 187
   || || || || || || || || || || || || || || || || || || || ||
Qy 166 LKSETLE-SEEFKRLHPYKSFIDTSLSG-----FDDQDLFGIWSKVVDPLFCESVH 218
   || || || || || || || || || || || || || || || || || || || ||
Db 188 YELATLEASSEFOALVRYRELLSYLTQNSGRVLSFIDAQYL-----NNTLFIEKLY 240
   || || || || || || || || || || || || || || || || || || || ||
Qy 219 NFTLPNSATEDAMIKUKELSELSSLXYGIHKQKSRLOGGVLYNEILK--NMKLATQP 276
   || || || || || || || || || || || || || || || || || || || ||
Db 241 NMTLPVWA--EKVGEKELTYVSNFAFSIATETRSMARLKTGPLLKDIFERFDKLNQNL 298
   : || || || || || || || || || || || || || || || || || || ||
Qy 277 QYKYLVMYSAHDTTVSGLMALDVYNGVLPYASCHMMEL-YHDKGGHFVEMYRYNETQ 335
   : || || || || || || || || || || || || || || || || || || ||
Db 299 KPDRSLWTYSAHDTTIANVLNSLKLFLHSPPYAACIMLEM RVDDSDNTPLVSFYKNTTA 358
   || || || || || || || || || || || || || || || || || || || ||
Qy 336 NEPYPLTLPGCTHSCPLEKFAELLDPIQDWATEC----NATSSHQGVTVGA 383
   || || || || || || || || || || || || || || || || || || || ||
Db 359 -EPLPLDIPGCGLSCLPLTLVKLYQDVLVFNWERECKRSTM MMTYEANLGA 409
   || || || || || || || || || || || || || || || || || || || ||

RESULT 8
O9U506 PRELIMINARY; PRT; 447 AA.
ID O9U506;
AC O9U506;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPH-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J51ST/100;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
```



DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
KW Hydrolase.  
SQ SEQUENCE 447 AA: 51049 MW: 10FABA5FAF6EEFF6 CRC64:

Query Match	31.4%;	Score 647;	DB 5;	Length 447;
Best Local Similarity	39.6%;	Pred. NO. 7e-46;		
Matches 147;	Conservative 64;	Mismatches 130;	Indels 30;	Gaps

Qy	373	ATSSHQCTVGA	383
	.	:	:
Db	399	MMTYEEANLGA	409

RESULT	10		
Q9U5T8			
ID	Q9U5T8	PRELIMINARY;	PRT; 447 AA.
AC	Q9U5T8;		
DT	01-MAY-2000	(Tremblrel. 13, Created)	
DT	01-MAY-2000	(Tremblrel. 13, Last sequence update)	
DT	01-MAR-2001	(Tremblrel. 16, Last annotation update)	
DE	ACID PHOSPHATASE-1 (EC 3.1.3.2).		
GN	ACPh-1.		
OS	Drosophila subobscura (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachytera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7241;		
[1]			
RN	SEQUENCE FROM N.A.		
RP	STRAIN=J4ST/054;		
RC	MEDLINE=99442390; Pubmed=10511564;		
RA	Navarro-Sabate A., Aguade M.; Segarra C.;		
RX	"the relationship between allozyme and chromosomal polymorphism		
RT	inferred from nucleotide variation at the Acph-1 gene region of		
RT	Drosophila subobscura.;"		
RL	Genetics 153:871-889(1999).		
RL	EMBL; AJ389445; CAB59943.1; .		
DR	HSSP: P15309; 2HPA.		
DR	FlyBase; FBgn0013885; Dsub\Acph-1.		
DR	InterPro; IPR000560; .		
DR	Pfam; PF00328; acid_phosphat; 2.		
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.		
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.		
KW	Hydrolase.		

SQ SEQUENCE 447 AA; 50982 MW; 5A320C40C4FE8803 CRC64;  
 Query Match 31.3%; Score 645; DB 5; Length 447;  
 Best Local Similarity 39.4%; Pred. No. 1e-45;  
 Matches 146; Conservative 65; Mismatches 130; Indels 30; Gaps 12;  
 QY 28 PQQAKELKFTLVFRHGRGPIETPTDPTITSS-WPQGFQLTQWMEQHYELGSYIRK 86  
 DB 54 PG--ELKFAHVFIRHGRDTPVDPTDPWNNRKFPTGWGQLTNLGKEQHYELGKWLRLN 110  
 QY 87 RYGRFLNDTYKHDQIYIRSTVDRTLMSAMTNLAALFPEGISINWRLLMQPIPVHTVS 146  
 DB 111 RYKSLGSRYTNEIDIFVQSTVDRTLMSAQSLAGLYEPQGGDIWNPRIWQPVVHTVP 170  
 QY 147 LSEDRLLYLPFRDPCRFELKSETLE-SEEFLLKRLHPYKSFSLDTLSSLSG-----FDDQ 199  
 DB 171 EKDDSLAAK-ASCPAY-DYELATLEASSEFOALYVRYRELLSYLTQNSGRVLKSFIDAQ 228  
 QY 200 DLFGIWSKYVDPLFCESVHNFTLPSWATEDAMIKLSELSELSSLLSLYGIHKOKESRLQG 259  
 DB 229 YL-----NNTLFTEKLYNMTLPWA--EKVYGKELTYVSNFAFSIATLTRSWARLKT 279  
 QY 260 GVLVNEILK--NMKLATQPKYKILVMYSAHDTTVSGLMALDVYNGVLPYPYASCHMEL 317  
 DB 280 GPLLKIDIFERFDKLNQKLPDRSLWIYSAHDTTIANVLNSLKLFLHSPPYAACIMLEM 339  
 QY 318 -YHDKGGHFVEMYRNETQNEPYPLTLCGTHSCPLEKFAELLDPVIFODWATEC----M 372  
 DB 340 RYDSDNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLKTLVKLYQDVLPGNWERECKRSTM 398  
 QY 373 ATSSHQGTGVA 383  
 DB 399 MMTYEANLGA 409  
 RESULT 11  
 QY05T5 PRELIMINARY; PRT; 447 AA.  
 AC QY05T5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
 GN ACPH-1.  
 OS Drosophila subobscura (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7241;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-J73(3+4)/100;  
 RX MEDLINE=99442390; PubMed=10511564;  
 RA Navarro-Sabate A., Aguade M., Segarra C.;  
 RT "The relationship between allozyme and chromosomal polymorphism  
 RT inferred from nucleotide variation at the AcpH-1 gene region of  
 RT Drosophila subobscura.";  
 RL Genetics 153:871-889(1999).  
 DR EMBL; AJ389457; CAB59955.1; -.  
 DR HSSP; P15309; 2HPA.  
 DR FlyBase; FBgn0013885; Dsub\AcpH-1.  
 DR InterPro; IPR000560; -.  
 DR Pfam; PF00328; acid\_phosphat; 2.  
 DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
 DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
 KW Hydrolase.  
 SQ SEQUENCE 447 AA; 51020 MW; 8EFA062C681B63A4 CRC64;

Query Match 31.3%; Score 645; DB 5; Length 447;  
 Best Local Similarity 39.4%; Pred. No. 1e-45;  
 Matches 146; Conservative 66; Mismatches 129; Indels 30; Gaps 12;

QY 28 PQQAKELKFTLVFRHGRGPIETPTDPTITSS-WPQGFQLTQWMEQHYELGSYIRK 86  
 DB 54 PG--ELKFAHVFIRHGRDTPVDPTDPWNNRKFPTGWGQLTNLGKEQHYELGKWLRLN 110  
 QY 87 RYGRFLNDTYKHDQIYIRSTVDRTLMSAMTNLAALFPEGISINWRLLMQPIPVHTVS 146  
 DB 111 RYKSLGSRYTNEIDIFVQSTVDRTLMSAQSLAGLYEPQGGDIWNPRIWQPVVHTVP 170  
 QY 147 LSEDRLLYLPFRDPCRFELKSETLE-SEEFLLKRLHPYKSFSLDTLSSLSG-----FDDQ 199  
 DB 171 EKDDSLAAK-ASCPAY-DYELATLEASSEFOALYVRYRELLSYLTQNSGRVLKSFIDAQ 228  
 QY 200 DLFGIWSKYVDPLFCESVHNFTLPSWATEDAMIKLSELSELSSLLSLYGIHKOKESRLQG 259  
 DB 229 YL-----NNTLFTEKLYNMTLPWA--EKVYGKELTYVSNFAFSIATLTRSWARLKT 279  
 QY 260 GVLVNEILK--NMKLATQPKYKILVMYSAHDTTVSGLMALDVYNGVLPYPYASCHMEL 317  
 DB 280 GPLLKIDIFERFDKLNQKLPDRSLWIYSAHDTTIANVLNSLKLFLHSPPYAACIMLEM 339  
 QY 318 -YHDKGGHFVEMYRNETQNEPYPLTLCGTHSCPLEKFAELLDPVIFODWATEC----M 372  
 DB 340 RYDSDNTPLVSVFYKNTTA-EPLPLDIPGCGLSCLPLKTLVKLYQDVLPGNWERECKRSTM 398  
 QY 373 ATSSHQGTGVA 383  
 DB 399 MMTYEANLGA 409  
 RESULT 12  
 QY05T2 PRELIMINARY; PRT; 447 AA.  
 AC QY05T2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE ACID PHOSPHATASE-1 (EC 3.1.3.2).  
 GN ACPH-1.  
 OS Drosophila subobscura (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7241;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-J80(3+4)/100;  
 RX MEDLINE=99442390; PubMed=10511564;  
 RA Navarro-Sabate A., Aguade M., Segarra C.;  
 RT "The relationship between allozyme and chromosomal polymorphism  
 RT inferred from nucleotide variation at the AcpH-1 gene region of  
 RT Drosophila subobscura.";  
 RL Genetics 153:871-889(1999).  
 DR EMBL; AJ389463; CAB59961.1; -.  
 DR HSSP; P15309; 2HPA.  
 DR FlyBase; FBgn0013885; Dsub\AcpH-1.  
 DR InterPro; IPR000560; -.  
 DR Pfam; PF00328; acid\_phosphat; 2.  
 DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; UNKNOWN\_1.  
 DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.  
 KW Hydrolase.  
 SQ SEQUENCE 447 AA; 50991 MW; 713B576FB0EC622E CRC64;

Query Match 31.3%; Score 645; DB 5; Length 447;  
 Best Local Similarity 39.6%; Pred. No. 1e-45;  
 Matches 147; Conservative 64; Mismatches 130; Indels 30; Gaps 12;

QY 28 PQQAKELKFTLVFRHGRGPIETPTDPTITSS-WPQGFQLTQWMEQHYELGSYIRK 86  
 DB 54 PG--ELKFAHVFIRHGRDTPVDPTDPWNNRKFPTGWGQLTNLGKEQHYELGKWLRLN 110  
 QY 87 RYGRFLNDTYKHDQIYIRSTVDRTLMSAMTNLAALFPEGISINWRLLMQPIPVHTVS 146

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Db 111 RYKSLGSRVTNEDIFVQSTDVDRTLMSAQSDLAGLYEPQGDIDWNPRIQWQPVVHTVP 170
QY 147 LSEDRLLYLPFRDPCPEELKSETLE-SEEFKLRLHYPKSFELDTLSLSG-----FDDQ 199
Db 171 EKDDSLAAK-ASCPAY-DYELATLEASSEFQALYVRYRELLSYLTQNSRLVKSFIQAQ 228
QY 200 DLFGINSKVYDPLFCESVHNFTLPSPWATEDAMIKKELSELSSLLSYGIHKQEKSRLOQ 259
Db 229 YL-----NNTLFIKLYNMTLPVMA--EKVYKKEELTVVSNFASFIAFTFSMARLKT 279
QY 260 GVLVNEILK--NKKLATOPQKYKKLVMSAHDTTVSGLOMALDVYNGVLPYPYASCHMMEL 317
Db 280 GPLLKDIFERFDKLNQLKPDRLSLMIYSAHDTTIANVLNSLKLFEVHSPPYAACIMLEM 339
QY 318 -YHDKGGHFVEMYRYNETONEPYPLTLPCTHSCPLKFAELLDVPIQDWATEC-----M 372
QY 340 RVDSNTPLSVFYKNTTA-EPLPLDIPGCGLSCLPLTKLVKLYQDVLPGNWERECKRSTM 398
Db 373 ATSSHQCTVGA 383
Db 399 MMTYEEANLGA 409
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## RESULT 13

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Q9U5T1
ID Q9U5T1 PRELIMINARY; PRT; 447 AA.
AC Q9U5T1;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
PT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPh-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J83(3+4)/100;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
inferred from nucleotide variation at the Acph-1 gene region of
Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL; AJ389466; CAB59964.1; -
DR HSSP; PI5309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\Acph-1.
DR InterPro; IPR000560; -
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51049 MW; 3C5F45BFA3FDC325 CRC64;
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Query Match 31.3%; Score 645; DB 5; Length 447;  
Best Local Similarity 39.1%; Pred. No. le-45;  
Matches 145; Conservative 67; Mismatches 129; Indels 30; Gaps 12;

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QY 28 PGQAKELKFVTLFRHGRDGRPIETFTDPTITESS-WPQFGQLTQMGMEQHYELGSYIRK 86
Db 54 PG---ELKFAHVIFRIGDRTVPDPTDPNNRKFWTGWLNTLKEQHYELGKWLNR 110
QY 87 RYGRFLNDTYKHQDIYIRSTVDVDRTLMSANTLAALFPPEGISIWNPRLLQPIPVHTVS 146
Db 111 RYKSLGSRVTNEDIFVQSTDVDRTLMSAQSDLAGLYEPQGDIDWNPRIQWQPVVHTVP 170
QY 147 LSEDRLLYLPFRDPCPEELKSETLESEEFKLRLH-YPKSFELDTLSLSG-----FDDQ 199
Db 171 EKDDSLAAK-ASCPAY-DYELATLESSEFQALYVRYRELLSYLTQNSRLVKSFIQAQ 228
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QY 200 DLFGINSKVYDPLFCESVHNFTLPSPWATEDAMIKKELSELSSLLSYGIHKQEKSRLOQ 259
Db 229 YL-----NNTLFIKLYNMTLPVMA--EKVYKKEELTVVSNFASFIAFTFSMARLKT 279
QY 260 GVLVNEILK--NKKLATOPQKYKKLVMSAHDTTVSGLOMALDVYNGVLPYPYASCHMMEL 317
Db 280 GPLLKDIFERFDKLNQLKPDRLSLMIYSAHDTTIANVLNSLKLFEVHSPPYAACIMLEM 339
QY 318 -YHDKGGHFVEMYRYNETONEPYPLTLPCTHSCPLKFAELLDVPIQDWATEC-----M 372
Db 340 RVDSNTPLSVFYKNTTA-EPLPLDIPGCGLSCLPLTKLVKLYQDVLPGNWERECKRSTM 398
QY 373 ATSSHQCTVGA 383
Db 399 MMTYEEANLGA 409
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## RESULT 14

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Q9TW17
ID Q9TW17 PRELIMINARY; PRT; 447 AA.
AC Q9TW17;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE-1 (EC 3.1.3.2).
GN ACPh-1.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RX MEDLINE=99442390; PubMed=10511564;
RA Navarro-Sabate A., Aguade M., Segarra C.;
RT "The relationship between allozyme and chromosomal polymorphism
inferred from nucleotide variation at the Acph-1 gene region of
Drosophila subobscura."
RL Genetics 153:871-889(1999).
DR EMBL; AJ389461; CAB59959.1; -
DR EMBL; AJ389450; CAB59948.1; -
DR EMBL; AJ389453; CAB59951.1; -
DR EMBL; AJ389454; CAB59952.1; -
DR EMBL; AJ389460; CAB59958.1; -
DR HSSP; PI5309; 2HPA.
DR FlyBase; FBgn0013885; Dsub\Acph-1.
DR InterPro; IPR000560; -
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 447 AA; 51006 MW; 3D3A6472A73B12E1 CRC64;
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Query Match 31.3%; Score 645; DB 5; Length 447;  
Best Local Similarity 39.4%; Pred. No. le-45;  
Matches 146; Conservative 66; Mismatches 129; Indels 30; Gaps 12;

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QY 28 PGQAKELKFVTLFRHGRDGRPIETFTDPTITESS-WPQFGQLTQMGMEQHYELGSYIRK 86
Db 54 PG---ELKFAHVIFRIGDRTVPDPTDPNNRKFWTGWLNTLKEQHYELGKWLNR 110
QY 87 RYGRFLNDTYKHQDIYIRSTVDVDRTLMSANTLAALFPPEGISIWNPRLLQPIPVHTVS 146
Db 111 RYKSLGSRVTNEDIFVQSTDVDRTLMSAQSDLAGLYEPQGDIDWNPRIQWQPVVHTVP 170
QY 147 LSEDRLLYLPFRDPCPEELKSETLE-SEEFKLRLHYPKSFELDTLSLSG-----FDDQ 199
Db 171 EKDDSLAAK-ASCPAY-DYELATLEASSEFQALYVRYRELLSYLTQNSRLVKSFIQAQ 228
QY 200 DLFGINSKVYDPLFCESVHNFTLPSPWATEDAMIKKELSELSSLLSYGIHKQEKSRLOQ 259
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 2, 2001, 18:19:06 ; Search time 13.14 Seconds  
(Without alignments)  
1003.681 Million cell updates/sec

Title: US-09-402-645-2

Sequence: 1 MGAAPLPSPATSLSLGFL.....DMATECMATSSHQGTGALG 385

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	88.2	381	1	P20646 ratlun norv
2	1848	88.2	381	1	P20646 ratlun norv
3	1848	88.2	381	1	P20646 ratlun norv
4	1848	88.2	381	1	P20646 ratlun norv
5	1848	88.2	381	1	P20646 ratlun norv
6	1848	88.2	381	1	P20646 ratlun norv
7	1848	88.2	381	1	P20646 ratlun norv
8	1848	88.2	381	1	P20646 ratlun norv
9	1848	88.2	381	1	P20646 ratlun norv
10	1848	88.2	381	1	P20646 ratlun norv
11	1848	88.2	381	1	P20646 ratlun norv
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25	1848	88.2	381	1	P20646 ratlun norv
26	1848	88.2	381	1	P20646 ratlun norv
27	1848	88.2	381	1	P20646 ratlun norv
28	1848	88.2	381	1	P20646 ratlun norv
29	1848	88.2	381	1	P20646 ratlun norv
30	1848	88.2	381	1	P20646 ratlun norv
31	1848	88.2	381	1	P20646 ratlun norv
32	1848	88.2	381	1	P20646 ratlun norv
33	1848	88.2	381	1	P20646 ratlun norv

## ALIGNMENTS

RESULT	ID	STANDARD	PRT	381 AA
1	PPAP_RAT			
AC	P20646			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).			
GN	ACPP.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90323620; PubMed=2373368;			
RA	Rolko K., Jaenke O.A., Vilko P.;			
RT	"Primary structure of rat secretory acid phosphatase and comparison to other acid phosphatases."			
RL	Gene 89:223-229(1990).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).			
RX	MEDLINE=93327749; PubMed=834986;			
RA	Schneider G., Lindqvist Y., Vilko P.;			
RT	"Three-dimensional structure of rat acid phosphatase."			
RL	EMBO J. 12:2609-2615(1993).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).			
RX	MEDLINE=94012606; PubMed=8407898;			
RA	Lindqvist Y., Schneider G., Vilko P.;			
RT	"Three-dimensional structure of rat acid phosphatase in complex with I(+)-tartrate."			
RL	J. Biol. Chem. 268:20744-20746(1993).			
CC	-1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN			
CC	ALCOHOL + ORTHOPHOSPHATE.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.			
CC	-----			
CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION			
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CC	OR SEND AN EMAIL TO <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: M33397; AAA41806.1; -			
DR	PIR: JH0152; JH0152.			
DR	PDB: 1RPA; 31-MAY-94.			
DR	PDB: 1RPT; 31-MAY-94.			
DR	InterPro: IPR000560; -			
DR	PIR: P000328; acid_phosphat.1.			
DR	PROSITE: PS00778; HIS_ACID_PHOSPHAT.2; FALSE_NEG.			
DR	PROSITE: PS00616; HIS_ACID_PHOSPHAT.1; 1.			
KW	Hydrolase; Glycoprotein; Signal; 3D-structure.			
FT	SIGNAL 1 31			

FT CHAIN 32 381 PROSTATIC ACID PHOSPHATASE.  
 FT DISULFID 160 371  
 FT DISULFID 346 350  
 FT ACT SITE 43 43  
 FT ACT SITE 85 85  
 FT CARBOHYD 93 93  
 FT CARBOHYD 219 219  
 FT CARBOHYD 332 332  
 FT CARBOHYD 381 AA: 43850 MM; 5EEBFF67B062FF67 CRC64;  
 SQ SEQUENCE

Query Match 88.3%; Score 1818; DB 1; Length 381;  
 Best Local Similarity 88.5%; Pred. No. 7.6e-137;  
 Matches 337; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

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 DB 1 MAAVPLHLVGTASTLTLGLFLLSLRLDPOAKELKFTLVFRRHGRGPRTEPTPTTES 60  
 QY 61 SMPQFGQLTQMGMDQHYELGSIYRKRGRFLNDTYKHDQIYIRSTVDVDTLMSANTNLA 120  
 DB 61 SMPQFGQLTKMGMDQHYELGSIYRKRGRFLNNSYKHDQIYIRSTVDVDTLMSANTNLA 120  
 QY 121 ALFPPREGISINWPRLLMOPPIVHTVSLSEDRLLYLPFRDCPRFOELKSEETLKSEFLKRL 180  
 DB 121 ALFPPREGISINWPRLLMOPPIVHTVSLSEDRLLYLPFRDCPRFOELKSEETLKSEFLKRL 180  
 QY 181 HPKYGFLLSLSGFDODLFGISKSYVDPLFCESVNHFTLPSNATEDAMIKELSEL 240  
 DB 181 QPKYGFIDTLPSLGSFEDODLFEIWSRLYDPLFCESVNHFTLRNATEDAMIKELSEL 240  
 QY 241 SLSLSYGIHKOKESKRLQGVLYNELKNMKTATOPQKYLKLVMSAHDTVSGLOMALD 300  
 DB 241 SLSLSYGIHKOKESKRLQGVLYNELKNMKTATOPQKYLKLVMSAHDTVSGLOMALD 300  
 QY 301 VYNGVLPYASCHMELTHDKGFVEWYRNETONEPPLTLPGCTHSCPLEKRAELLD 360  
 DB 301 LVNGVLPYASCHMELTHDKGFVEWYRNETONEPPLTLPGCTHSCPLEKRAELLD 360  
 QY 361 PYIPDMATECMATSSHOQTV 381  
 DB 361 PYIPDMATECMATSSHOQTV 381

RESULT 2  
 PPAP\_HUMAN STANDARD: PRT: 386 AA.  
 AC P15309;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).  
 GN ACP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92272747; PubMed=1375464;  
 RA Sharief F.S., Li S.S.-L.;  
 RT "Structure of human prostatic acid phosphatase gene."  
 RL Biochem. Biophys. Res. Commun. 184:1468-1476(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, DISULFIDE BONDS, & ACTIVE SITE.  
 RX MEDLINE=91115848; PubMed=1989985;  
 RA van Etten R.L., Davidson R., Stevis P.E., MacArthur H., Moore D.L.;  
 RT "Covalent structure, disulfide bonding, and identification of  
 RT reactive surface and active site residues of human prostatic acid  
 RT phosphatase."  
 RL J. Biol. Chem. 266:2313-2319(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=89228054; PubMed=2712834;  
 RA Sharief F.S., Lee H., Leuderman M.M., Lundwall A., Deaven L.L.,  
 RA Lee C.-L., Li S.S.-L.;  
 RT "Human prostatic acid phosphatase: cDNA cloning, gene mapping and  
 RT protein sequence homology with lysosomal acid phosphatase."  
 RL Biochem. Biophys. Res. Commun. 160:79-86(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX TISSUE=Prostate;  
 RC MEDLINE=88312981; PubMed=2842184;  
 RA Viikio P., Viikonen P., Henttu P., Roiko K., Solin T., Huhtala M.L.;  
 RT "Molecular cloning and sequence analysis of cDNA encoding human  
 RT prostatic acid phosphatase."  
 RL FEBS Lett. 236:275-281(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Prostate;  
 RC MEDLINE=90370491; PubMed=2395659;  
 RA Tallor P.G., Govindan M.V., Patel P.C.;  
 RT "Nucleotide sequence of human prostatic acid phosphatase determined  
 RT from a full-length cDNA clone."  
 RL Nucleic Acids Res. 18:4928-4928(1990).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95038536; PubMed=7951074;  
 RA Sharief F.S., Li S.S.-L.;  
 RT "Nucleotide sequence of human prostatic acid phosphatase ACP gene,  
 RT including seven Alu repeats."  
 RL Biochem. Mol. Biol. Int. 33:561-565(1994).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=99023966; PubMed=9804805;  
 RA Lacount M.W., Handy G., Lebioda L.;  
 RT "Structural origins of L(+)-tartarate inhibition of human prostatic  
 RT acid phosphatase."  
 RL J. Biol. Chem. 273:30406-30409(1998).  
 CC -I- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN  
 CC ALCOHOL + ORTHOPHOSPHATE.  
 CC -I- SUBUNIT: HOMODIMER.  
 CC -I- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.  
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 CC -----  
 CC DR EMBL; M97589; AAA60021.1; -;  
 CC DR EMBL; M97580; AAA60021.1; JOINED.  
 CC DR EMBL; M97581; AAA60021.1; JOINED.  
 CC DR EMBL; M97582; AAA60021.1; JOINED.  
 CC DR EMBL; M97583; AAA60021.1; JOINED.  
 CC DR EMBL; M97584; AAA60021.1; JOINED.  
 CC DR EMBL; M97585; AAA60021.1; JOINED.  
 CC DR EMBL; M97586; AAA60021.1; JOINED.  
 CC DR EMBL; M97587; AAA60021.1; JOINED.  
 CC DR EMBL; M97588; AAA60021.1; JOINED.  
 CC DR EMBL; M34840; AAA60021.1; JOINED.  
 CC DR EMBL; M24902; AAA60022.1; -;  
 CC DR EMBL; X52174; CAA36422.1; -;  
 CC DR EMBL; X53605; CAA37673.1; -;  
 CC DR EMBL; U07097; AAB60640.1; -;  
 CC DR EMBL; U07083; AAB60640.1; JOINED.  
 CC DR EMBL; U07085; AAB60640.1; JOINED.  
 CC DR EMBL; U07086; AAB60640.1; JOINED.  
 CC DR EMBL; U07088; AAB60640.1; JOINED.  
 CC DR EMBL; U07091; AAB60640.1; JOINED.  
 CC DR EMBL; U07092; AAB60640.1; JOINED.  
 CC DR EMBL; U07093; AAB60640.1; JOINED.  
 CC DR EMBL; U07095; AAB60640.1; JOINED.  
 CC DR PIR; A32419; A32419.







OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9350910; PubMed=2764916;  
 RA Himeno M., Fujita H., Noguchi Y., Kono A., Kato K.;  
 RT "Isolation and sequencing of a cDNA clone encoding acid phosphatase  
 in rat liver lysosomes.";  
 RL Biochem. Biophys. Res. Commun. 162:1044-1053(1989).  
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN  
 CC ALCOHOL + ORTHOPHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: LYSOSOMAL.  
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M27893; AAA40744.1; -  
 DR PIR: A33395; A33395.  
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 DR InterPro: IPR000560; -  
 DR Pfam: PF00328; acid\_phosphat; 1.  
 DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
 DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
 KW Hydrolyase; Signal; Glycoprotein; Lysosome.  
 FT SIGNAL 1 30  
 FT CHAIN 1 423  
 FT DISULFID 159 370  
 FT DISULFID 212 310  
 FT DISULFID 345 349  
 FT ACT\_SITE 42 42  
 FT ACT\_SITE 84 84  
 FT ACT\_SITE 286 286  
 FT CARBOHYD 92 92  
 FT CARBOHYD 133 133  
 FT CARBOHYD 167 167  
 FT CARBOHYD 177 177  
 FT CARBOHYD 191 191  
 FT CARBOHYD 197 197  
 FT CARBOHYD 267 267  
 FT CARBOHYD 322 322  
 FT CARBOHYD 331 331  
 SQ SEQUENCE 423 AA; 48319 MW; 6F4C4819CADD4496 CRC64;  
 Query Match 49.5%; Score 1019.5; DB 1; Length 423;  
 Best Local Similarity 51.9%; Pred. No. 1.6e-73;  
 Matches 189; Conservative 61; Mismatches 109; Indels 5; Gaps 3;  
 Oy 21 LLSLCL---DGGQAKELKFTYLVRRHGRGPIETFPDPTIETSSMPGFGQLTOMGEQH 77  
 Db 17 LLLGSLAMPPIQARSIRFVTLRHGDRSPKAVPRDPVOEEKMPGFGQLTKEGMLQH 76  
 Oy 78 YELSGYTRKRGFRPLNDYTKHDOYIRSTVDYFRLMSAMTALALPPEGSIINPRLLW 137  
 Db 77 WELGQALRQRHGFGLNMYNHOEYVASTDTRILMSAEALALPPTPEYQHNPNISW 136  
 Oy 138 QPIPVHTVSLSEDRLLYLPFRDCPRFELKSETLSESEFRLRLPYKSFLLDTLSLSGFD 197  
 Db 137 QPIPVHTVLPTEEDRLKFLGRCPRYEQLOQNETQOTPEYQMSIQNOQFLMVAENEGIM 196  
 Oy 198 DQDLFGIMSKYDPLFCESVNFPLPSWATDAMIKELSELISLSTYGHKREKESRL 257  
 Db 197 NLLETITWN-VYDPLFCFQTHGLLPPWASPOTVOALSQLDPSFLFLFGTHDVOYKARL 255  
 Oy 258 QGVLVNEILKMKLALQPKYKRLVMSAHDITVSGLOMLADVYNGVLPYASCHMMEL 317

Db 256 QGVLVLAQILKLNLTMTTQFRLVYSADHTLVALQALNLYNKKQAPYASCHIFEL 315  
 Oy 318 YHDKGHP-VEMYRYNFTQNEPPYPLTLPCTHSCPLEFAELDPVLPDWMATECMATSS 376  
 Db 316 YQEDNGNEVSVMYFRNDSKAPMPLTLPGCPHRCPLDPLRTEPVIIPKDMQKCCQLASD 375  
 Oy 377 HQGT 380  
 Db 376 TADT 379  
 RESULT 6  
 ID PPAT\_CAEEL STANDARD; PRT; 411 AA.  
 AC Q10944;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE POTATIVE ACID PHOSPHATASE B0361.7 PRECURSOR (EC 3.1.3.2).  
 GN B0361.7.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peleiderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Du Z.;  
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN  
 CC ALCOHOL + ORTHOPHOSPHATE.  
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.  
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 CC -----  
 DR EMBL: U00031; AAA50626.1; -  
 DR HSSP: P20646; 1RPT.  
 DR WormRep: B0361.7; CE00836.  
 DR InterPro: IPR000560; -  
 DR Pfam: PF00328; acid\_phosphat; 2.  
 DR PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
 DR PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
 KW Hypothetical protein; Signal; Glycoprotein; Hydrolyase.  
 FT SIGNAL 1 13  
 FT CHAIN 1 411  
 FT ACT\_SITE 40 40  
 FT ACT\_SITE 80 80  
 FT ACT\_SITE 278 278  
 FT ACT\_SITE 363 363  
 FT DISULFID 152 302  
 FT DISULFID 205 302  
 FT CARBOHYD 338 342  
 FT CARBOHYD 104 104  
 FT CARBOHYD 210 210  
 FT CARBOHYD 218 218  
 FT CARBOHYD 312 312  
 FT CARBOHYD 323 323  
 SQ SEQUENCE 411 AA; 47110 MW; BA265D808EC8B11C CRC64;  
 Query Match 26.3%; Score 542.5; DB 1; Length 411;  
 Best Local Similarity 34.7%; Pred. No. 1e-35;  
 Matches 135; Conservative 61; Mismatches 138; Indels 55; Gaps 14;  
 Oy 19 LLLSLCLD-----PGQAK--ELKFTYLVRRHGRGPIETFPDPTIETSSMPQ 64  
 Db 2 LLLVLLIGASGINAVYKVEPIQANDTLEYVHTVRRHGRDPAELLPDDITK--WPE 59

RESULT	7
PPAX_CAEEL	STANDARD; PRT; 755 AA.
ID	PPAX_CAEEL
AC	Q09549; Q17843;
DT	01-NOV-1995 (Rel. 32, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	PURATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).
GN	F26C11.1.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC	Rhabditidae; Pelodierinae; Caenorhabditis.
OX	NCBI_TaxId=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BRISTOL N2;
RA	Matthews P., Lloyd C.;
RL	Submitted (NOV-1998) to the EMBL/Genbank/DBD databases.
CC	-1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
CC	ALCOHOL + ORTHOPHOSPHATE.
CC	-1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC	-----
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CC	or send an email to <a href="mailto:license@lsb-sib.ch">license@lsb-sib.ch</a> ).
CC	-----
DR	EMBL; 247072; CAAB7370.1; -
DR	EMBL; 254342; CAAB7370.1; JOINED.
DR	EMBL; 254342; CAAB7370.1; -
DR	EMBL; 247072; CAAB7370.1; JOINED.
DR	Mormep; F26C11.1; CE05732.
DR	InterPro: IPR000560; -
DR	Pfam; PF00328; acid_phosphat; 1.
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KM	Hypothetical protein: Hydrolyase.
FT	ACT_SITE 356 356 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT	ACT_SITE 359 399 BY SIMILARITY.
FT	ACT_SITE 636 636 PROTON DONOR (BY SIMILARITY).
FT	DISULF 702 708 BY SIMILARITY.
SO	SEQUENCE 755 AA; 87783 MW; E7F3050115A235EB CRC64;

Query Match	15.0%	Score 310:	DB 1:	Length 755:	
Best Local Similarity	26.7%	Pred. NO. 6e-17:			
Matches 112:	Conservative	65:	Mismatches 148:	Indels 94:	
				Gaps 16:	
QY	33	ELKPYTLVFRHDDRCPRIEFPPDPTTSSWP----	GGFGOLTQWGMEOHYELGSIYIRKRY-	88	
Db	346	KLEFVQTIWRHGRDSALBEL--	FPISSEKMTWTFGGGGLGELTFPMGSEMMNIGITRRRRY	403	
QY	89	--GRLNDTYKHKDQIYIRSTVDYDRFLMSAMTUALAFPEEGISTMNP-			
Db	404	EDQGLPSHHYAAKELEYIRSTNLNRLIISMSLIYGMFP-	--GAWNIGQVDYDPNDVDMQO	460	
QY	140	----IPVHTVSLSEDRLLYLPDPCDPREELKSE-----			
Db	461	GFTFLPVHNDGI--	DQCAVAOLCNRRCPELOEKMAELEDVKNATVAMIALNRRAALYN	518	
QY	170	-TLESEELKRLAPYKS----	FLDTLSLSLGFDDDLFGIMSKYVDPLECESVHNFTLPS	224	
Db	519	VYDQEKERKRYTDAMCKQHMFNDPMDYOOPLPMYNEGLIDVNAORTYAPKRFTEGNFGNPK		578	
QY	225	WATEPAMIRKLKELSELSELSTLGYIHOKRKSLOGGVLYNELTKMMK-----	LA	273	
Db	579	PSIVD-----	GDIIPQEVSTLGGGPLNELTEFENGREKIRCVADAENCS	621	
QY	274	TQPKRYKLLVMYSAHDTTVSGLOMALDYVNGV-----	LPPIYASCHMELIYHDKGSH--	327	
Db	622	IDYLPKRFYAVASSHDOLYALLVLTGITDYVKTVGDGMDPTSSLTILEYSSNPGQSSVK		681	
QY	328	MYRNETQNEPPLP--	LPGCTHS--	CPLKRAEALLDPIIP--QDMATECMATSSHQGIY	381
Db	682	FLYRNSNDNFSDVYSQIPVCGNADYCAASDQNTAYOFKPLPDVWTLCENSLSSISSY		740	

```

RESULT      8
PPAW_CAEEL ID_PPAW_CAEEL STANDARD: PRT; 413 AA.
AC 009451;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PURATIVE ACID PHOSPHATASE C05C10.4 (EC 3.1.3.2).
GN C05C10.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdillida; Rhabditidae;
OC Rhabdillidae; Pelodertinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN (1)
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL NZ;
RC STRAIN-BRISTOL NZ;
RA Matthews P.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN (2)
RN REVISIONS.
RP STRAIN-BRISTOL NZ;
RC STRAIN-BRISTOL NZ;
RA Jones S.J.M.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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CC -----
DR EMBL; Z48178; CA88205.1; -.
DR WormPep; C05C10.4; CE17370.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.

```



RL J. Bacteriol. 172:802-807(1990).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655.  
 RX MEDLINE:97426617; PubMed-9276503.  
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.:  
 RT "The complete genome sequence of *Escherichia coli* K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE-97061202; PubMed-8905232;  
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kojihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizouchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,  
 RA Samped G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiiuchi T.:  
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome  
 corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996).  
 RN [4]  
 RP SEQUENCE OF 23-34.  
 RC STRAIN-K12 / EMG2;  
 RX MEDLINE-97443975; PubMed-929846;  
 RA Link A.J., Robison K., Church G.M.:  
 RT "Comparing the predicted and observed properties of proteins encoded  
 in the genome of *Escherichia coli* K-12.";  
 RL Electrophoresis 18:1259-1313(1997).  
 CC -1- FUNCTION: ABSOLUTELY REQUIRED FOR THE GROWTH OF E. COLI IN A HIGH-  
 CC PHOSPHATE MEDIUM CONTAINING G-1-P AS THE SOLE CARBON SOURCE.  
 CC -1- CATALYTIC ACTIVITY: D-GLUCOSE 1-PHOSPHATE + H(2)O -> D-GLUCOSE +  
 CC ORTHOPHOSPHATE.  
 CC -1- ENZYME REGULATION: INDEPENDENT FROM INORGANIC PHOSPHATE  
 CC AVAILABILITY, AND APPARENTLY SUBMITTED TO CATABOLITE REPRESSION,  
 CC IT IS POSITIVELY CONTROLLED BY CAMP AND THE CAMP RECEPTOR PROTEIN.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.  
 CC -1- MISCELLANEOUS: OPTIMALLY ACTIVE AROUND PH 4.  
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.  
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 CC -----  
 CC EMBL; M3807; AAA23426.1; -;  
 CC EMBL; AE000202; AAC74087.1; -;  
 CC EMBL; D90737; BAA35769.1; -;  
 CC EMBL; D90738; BAA35779.1; -;  
 CC PIR: JY0087; JY0087.  
 CC ECGene: EG10033; app.  
 CC InterPro: IPR000560; -;  
 CC Pfam: PF00328; acid\_phosphat; 1.  
 CC PROSITE: PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
 CC PROSITE: PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.  
 CC Hydrolase; Periplasmic; Signal.  
 CC SIGNAL  
 CC CHAIN 1 22  
 CC FT 23 413 GLUCOSE-1-PHOSPHATASE.  
 CC FT ACT\_SITE 40 40 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).  
 CC FT ACT\_SITE 311 311 PROTON DONOR (BY SIMILARITY).  
 CC SEQUENCE 413 AA; 45683 MW; A0ADAD3639DD6AB C6C64;

```

Oy 12 ASLSGFLFLLSLCLDPCQA-----ELKFVTLVFRHGRGPLETPT--DPTESMP 63
Db 7 AAAAAGIYLLAS-----NAQAOTVEGQLODQVLMMSKRNLRAPLANNGSVLEOSTPKWP 62
Oy 64 Q--GEGOLTWGMEOHYELGSYTRKRYGRFLANDTYKHDO-----LYIRSTDVRTLMS 114
Db 63 EMDYPGQGLTTKGGVLEYYMGHYRMLAE--QGMVKSGECPPTYVAYANSLOFTVAT 120
Oy 115 AMTNIALAFPEEGISINNRPILMOPRIYHYHVSLEDRLLLPFDPCRFEEL-KSETLES 173
Db 121 AOFETFGAFPCDIPVNHQEMKGTMDPTFNVIYTDSDSAASEQAVAAAMEKELSKLOLTD 180
Oy 174 EEPFLKRLAPRYK-----SFLDILLSLGFDDO-----LFGIMSVYDOPFCESV 217
Db 181 YOLLERYIYNDDSPACKKEQOCSLVDCGNFTFSAKYQOEPPVSGPLKAGNSLVDFTLQY 240
Oy 218 HNFTLP--SWATEDAMIKLELSELSLSLSTLYGIKREKSEKSLQGVLYNEILNMKLATQ 275
Db 241 EGFPRPDQYVAWEIISDQOQWYKLLKNGYOQSLTSPSEVARNNAKPLVSYIDK--ALVTD 298
Oy 276 POKIKKLVMIYSAHDTYVSGLOMALDYINGVLPPYASCH-----MMELYHDKG 323
Db 299 RTSAPKIVLVGHSDNISLSTALD-----FKPY-QLHDONERTPIGKIYVFRMHDSKA 352
Oy 324 H-----EVEMYVRNENQ-----NEPYLTLRGCHTS-----GRLKPAELLDPVI 365
Db 353 NNDLMIKEYVQSEQLRNADALTLOAPQAQVYLTLESGCPIDADGCPMKQFSDVLEAV 412

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ID	VE02_VACC	STANDARD:	PRT:	737 AA.
AC	P21080;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-FEB-1991 (Rel. 17, Last annotation update)			
DE	PROTEIN E2.			
GN	E2L.			
OS	Vaccinia virus (strain Copenhagen).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.			
CC	NCBI_TaxID=10249;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91021027; PubMed=2219722;			
RA	Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P., Paoletti E.;			
RT	"The complete DNA sequence of vaccinia virus.";			
RL	Virology 179:247-266(1990).			
RN	[2]			
RP	COMPLETE GENOME.			
RA	Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P., Paoletti E.;			
RL	Virology 179:517-563(1990).			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
EMBL	M35027; AAA48039.1; -.			
DR	PIR; F42508; F42508.			
SO	SEQUENCE 737 AA; 85916 MW; A4DBE8BA1BFCC2E2F4 CRC64;			

Query Match	5.98;	Score 121;	DB 1;	Length 413;
Best Local Similarity	20.0%;	Pred. No. 0.025;		
Matches	84;	Conservative	70;	Mismatches 184;
				Indels 82;
				Gaps 17

Query Match	5.68;	Score 115.5;	DB 1;	Length 737;
Best Local Similarity	21.58;	Pred. No. 0.15;		
Matches	83;	Conservative	67;	Mismatches 125;
			Indels	111;
			Gaps	21;

```

QY 10 PTLISLGFLLLSLCLDPCGAKLKFVTLVFRIGDGRPIETE---PTDITESSWQGF 66
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 350 PVTSLPHSTLWVMCI-----OMKIVDIY-ELDEIDIDTLIEKGDPIETETE--- 389
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 GOLTQMGEOHQHYELGASYIRKRYG-----RFLND---TYKHQDIYRSTDVDVTRTMSAM 116
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 399 ---TTRW-YKNHNDITILYIKKYGCPMMKRMFEYPLTREADSHLLKTTMDENRG----- 450
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 TNLALFPPPGIS-----IWNRLMOPIV---HTVSLSEDRLLYLPFRDCPFEE 165
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 451 ---AIMEFPPTICLPYLLCCNMYKLKORPIPFKEENRNIIYKKKNRVL-----C-FDS 499
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 166 LKSFTESEEFKRLHMYKSFLOTLSSLSGDDODLFGIMSKYVDLFC-----ESVH 219
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 500 LENSAPF-----LKRIDSIPGLKTYNMMDIYENSNNILCVRFPOESIH 546
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 220 PTLSPMATEDAMIKLKEISELSLXGINKHOKERSKLOGVLVNEILKMKMLATOPQY 279
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 547 -----EERKRL-QLFDIARLASGVIYPSRYLSSMTPVYNNM--EGRETTNOKI 595
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 280 KKLIV---MYSAH-----DTVYSGLOMALDYVNGVLPY---ASCNME 316
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 596 ECLVILLDFSEEFLEYONIGNAVSNKRYELETTISNYOALINCLMSTLLIYLGSIIRSIS 655
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 317 LYHDKGHFVEMYR-----NFTQNEP 338
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 656 KTEBPFVUSILNIFYKGUKINLITSEP 681
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT	12
VE02_VACCV	
ID	VE02_VACCV
STANDARD;	
PRT;	737 AA

DT	01-MAY-1991	(Rel. 18, Created)
DT	01-NOV-1991	(Rel. 20, Last sequence update)
DT	01-NOV-1991	(Rel. 20, Last annotation update)
DE	PROTEIN E2.	

OS Vaccinia virus (strain WR).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX  
NCBI\_TaxID=10254;

RP SEQUENCE FROM N.A.  
RA Gershon P.D., Jones E.V., Moss B., Ahn B.-Y.;  
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases

RP	SEQUENCE OF 1-597 FROM N.A.
RX	MEDLINE=90377234; PubMed=2398897;

\* Identification of rpo30, a vaccinia virus RNA polymerase gene with

Factor.?  
Mol. Cell. Biol. 10:5433-5441 (1990).

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DR EMBL; M36339; AAB59822.1; -.  
DR PIR; A35928; A35928.  
SQ SEQUENCE 737 AA; 85957 MW; D5BAF09E2F944A9E CRC64

Query Match	5.4%	Score 110.5;	DB 1;	Length 737;
Best Local Similarity	21.2%;	Pred. No. 0.37;		
Matches 82;	Conservative	68;	Mismatches 125;	Indels 111;
				Gaps 21.
OY	10	PTASISGIFLLISICLDPGQAKELKFTYLVFRHDDRGPIETF---	PPIDPTRESSPGQCF	66

```

Db 350 PVTSLPHISTIVAMWCI-----OMKIYDVI-ERLDEIDIDTLIEKADPITTEYTF-----3989
QY 67 GOLTQMEQHOHYELGSYIRKRYG-----RELND-----TYKHQDIYTRSDVDVTRTMSAM 116
Db 399 ---TRW-YNKINDILITLYIKRYGCPMMKRLMEFYLPTEASDHLLKTADENRG-----450
QY 117 TNLALPPEGIS-----INPRLLWQIPV-----HTVSLSEDRLLYLPFRDCPREE 165
Db 451 ---AIMFPRITCPLPYLCCNYKLIKQPIPEKRENNIYKKNNRVL-----C-FDS 499
QY 166 LKSETLESEEPFLKRLHPKSFLOTLSSLSGFDODLFGIMSKYDPLFC-----ESVHN 219
Db 500 LENSAFKS-----LIKIDSIPLKATYNNMIDITEKSNITICVAFIPOSISHN 546
QY 220 FTLPDMATEDAMIKLELSELSSLISLYGIRKQKSKRLOGCVLNETLKNMKTQPOKY 2179
Db 547 -----EERIRKL-QLFDIARLASGYIIPSRYSLSMTVPVNM1--EGRETYNPOKI 5959
QY 280 KKLW---MYSAH-----DITVSGLOMALDYNVNGVLPVY---ASCHIME 316
Db 596 ECLVILDLFSEEFLEYONLGNVAENKYELETYISNYOAINCMJSTLILLYLGISIRIS 6555
QY 317 LYHDGGHFVEMYR---NETONEP 338
Db 656 RTENFVLSILNIFYGKLKINELLESEP 681

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RESULT	13
RRPO PEAMV	

ID	RRPO_PEAHV	STANDARD;	PRT;	599 AA
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DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48).

OS Pea enation mosaic virus (PEMV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae.  
OC Enamovirus.  
OX NCBI\_TaxID=12290;

RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=WSG;
RX	MEDLINE=91341468; PubMed=1875194;

RA Demiers A., de Zooten G.A.: "The nucleotide sequence and luteovirus-like nature of RNA 1 of an RT aphid non-transmissible strain of pea enation mosaic virus."; *J. Gen. Virol.* 72:1819-1834(1991).

CC -1- STIMULANT: 10 LATEOVIRUS RNA-DIRECTED RNA POLYMERASES.  
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DR EMBL; L04573; AAA72297.1; ALT\_INIT.  
DR PIR; J01384; RRRBPM.  
DR Interpro: IPRO001795; -  
DR Pfam; PF02123; Luteo\_ORF3\_1.  
DR PRINTS; PR00914; LVIRSRNBPOL.  
DR Trnsterase; RNA-directed RNA polymerase

ET	VARIANT	66	66	Q -> P.
ET	VARIANT	78	78	G -> S.
ET	VARIANT	84	84	S -> I.
ET	VARIANT	93	93	T -> I.
ET	VARIANT	95	95	R -> G.
ET	VARIANT	104	104	R -> L.
ET	VARIANT	336	336	V -> H.
ET	VARIANT	359	359	I -> I.
ET	VARIANT	410	410	S -> F.





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